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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

geneseqp1980s:* geneseqp1990s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003as:* A_Geneseq_29Jan04:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMAKIES	
	Score	ت ته	Length	DB	ID	Description
-	65	100.0	12	5	AAY32789	
0	65	100.0	130	0	AAY32792	
m	65	100.0	637	Н	AAP92108	
4	65	100.0	638	Н	AAP81326	92
· LO	65	100.0	638	н	AAP81327	7
9	65	100.0	638	M	AAP92107	07
7		100.0	638	~	AAW33394	4
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6		100.0	638	7	ADD45061	
10	65	100.0	638	7	ADD45067	Add45067 Human Pro
11		100.0	638	7	ADD45063	m
12		100.0	63.8	7	ADD45065	Ŋ
13	65	100.0	648	4	ABB11437	7 Human
14	61	93.8	638	7	AAR06473	
15	5.5	90.8		7	AAY32794	4 Chicken
16	59	90.8	608	7	AAR25246	
17	53	81.5		7	AAY32793	_
18	48	73.8	1399		ABU41685	ın
19	48	73.8	1409	9	ABU39890	0
20	4.5	69.2			ABB77350	
21	40		193	m	AAG60096	G
22	40	61.5	203	٣	AAG60095	Ŋ.
23	40	61.5	251	9	ABM69113	Photor
24	40		1363	4	AAB37607	7
25	40	61.5	1363	9	ABU04285	Abu04285 Human exp

	Ada09064 Lanthanid	Aaw20448 H. pylori	Aab53166 Macaca mu	Aaw20847 H. pylori	Abb58263 Drosophil	Adc97612 E. faeciu	Abm70226 Photorhab	Abb70491 Drosophil	Aau33683 Pseudomon	Abul5652 Protein e		Aag40846 Zea mays	Aag43965 Zea mays		Adc00980 Enterohae	Abb05007 Human ree	Ade60143 Human Pro	Abb05008 Mouse ree	Abb57065 Mouse isc
ABB48962	ADA09064	AAW20448	AAB53166	AAW20847	ARR58263	ADC97612	ABM70226	ABB70491	AAU33683	ABU15652	AAG43966	AAG40846	AAG43965	ABP66339	ADC00980	ABB05007	ADE60143	ABB05008	ABB57065
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ALIGNMENTS

XX XX Growth hormone receptor polypeptide for inhibition of receptor cleavage. XX XX KW Growth hormone receptor; signal transduction; proteolytic cleavage; KW uniquitin; proteosome binding site; muscle wasting; renal tubular defect; XX
9961-0HD-00 HD

98EP-00200799. 98EP-00200799. (UYUT-) RIJKSUNIV UTRECHT. 12-MAR-1998; 12-MAR-1998;

WPI; 1999-510568/43.

Claim 11; Page 27; 36pp; English.

Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

This sequence is from the intracellular domain of the growth hormone receptor. This sequence is an example of a binding site motif AAY32790.

This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptors being present on the surface for longer and therefore in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding contif, of which this sequence is an example, is located at or around a cubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as remal tubular defects, uraemia, associated with disorders such as remal tubular defects, uraemia, after diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after

AAP92108 standard; protein; 637 AA.

RESULT 3 AAP92108

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Gaps

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Length 12;

Score 65; DB 2; Length 12, Pred. No. 0.00043;

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63

52 DSWVEFIELDI

q

Human growth hormone receptor.

Growth hormone receptor.

Homo sapiens

US4857637-A.

(first entry)

14-FEB-1990

AAP92108;

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Signal transduction; proteolytic cleavage; growth hormone receptor; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency.
                                                                                                                                                                                                                                                                                                                                                                             Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
stress and during neuromuscular disease
                                                                                                                                                                                       Growth hormone receptor polypeptide.
                                                                                                                                 AAY32792 standard; peptide; 130 AA.
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                                   100.0%;
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                                                     12; Conservative
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                                             Local Similarity
                  Sequence 12 AA;
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                                   Query Match
                                                    Matches
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Modulating growth hormone receptor activity - by immunising animal against growth hormone receptor extracellular domain deriv. to rai antisera.

Disclosure; Fig 2a-c; 18pp; English.

Wood WI;

Spencer SA,

Martin DW,

Hammonds RG, Leung DW,

WPI; 1989-300419/41. N-PSDB; AAN91325

(GETH) GENENTECH INC.

87US-00061942.

12-JUN-1987; 22-MAY-1985; 07-MAY-1986;

15-AUG-1989.

86US-00861236 85US-00737302

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This sequence is a growth hormone receptor polypeptide. Polypeptides for the upregulation of the growth hormone receptor are derived from this sequence e.g. AAN32793. Variants (AAN32794-Y32823) of the derived from this sequence e.g. AAN32793. Variants (AAN32794-Y32823) of the derived to sequence e.g. AAN32793. Variants (AAN32794-Y32823) of the derived controlling proteosome binding site located on the intracellular part of a cell surface receptor. These sequences are used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this controlling proteolytic cleavage of the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which can might be present. The inhibitor is either derived from, competes with or binds to a polypeptide sequence of which sequences AAY32794-Y33823 are complete. The inhibitor may be used to treat muscle wasting, associated contains a sensiting disorders, AIDS, after stress and Anvier Anivernal Andal Anvier Aniversal and Anvier Aniversal Andal Aniversal Andal Aniversal Andal Aniversal Andal Aniversal Andal Aniversal Andal Aniversal Ani
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100.0%; Pred. No. 0.0056;
Live 0; Mismatches 0; Indels
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An animal can be immunised against its growth hormone receptor by vaccinating against a growth hormone receptor extracellular domain deriv. predetermined to raise polyclonal antisera which affect the receptor as a growth hormone agonist. This method enables continuous growth of target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; gigantism; acromegaly.
                                                                                                                                                                                                                                                                                                                        tissues without frequent hormone admin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP81326 standard; protein; 638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human growth hormone receptor,
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Matches 12; Conservative
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Conservative

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New pure growth hormone receptor and binding protein - for ty growth hormone abnormalities, and new encoding DNA sequences
                                   Disclosure; Page ?; 1pp; English.
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86US-00861236.
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Matches 12; Conservative
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                                                                                                                                       Query Match
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                                                                                                                                                                                                                                   disorders such as gigantism and acromegaly. A hydropathy plot revealed an extracellular GH binding domain, a transmembrane domain, and an intracellular signalling domain. Eight potential N-linked glycosylation sites are predicted. See also AAP81327 and AAN81718-9
                                                                                                                                                                                                        The sequence was deduced from a clone isolated from an adult liver cDNA lambda gt10 library. The DNA can be inserted into an expression vector for prodn. of the recombinant GHR which is used to treat GH-related
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                           New pure growth hormone receptor and binding protein - for treating growth hormone abnormalities, and new encoding DNA sequences.
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/label= signal_sequence
   /label= signal_sequence
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N-PSDB; AAN81717.
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nes 12; Conserv
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The sequence was deduced from a clone isolated from a rabbit liver cDNA lambda gtll library. The DNA can be inserted into an expression vector for prodn. of the recombinant GHR which is used to treat GH-related disorders such as gigantism and acromegally. A hydropathy plot revealed an extracellular GH binding domain, a transmembrane domain, and an intracellular signalling domain. Eight potential N-linked glycosylation sites are predicted. See also AAP81326 and AAN81718-9
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100.0%; Pred. No. 0.031;
cive 0; Mismatches 0;
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AAW33395 standard; protein; 638 AA.

AAW33395 RESULT

339 DDSWVEFIELDI 350 DDSWVEFIELDI 12

à d (first entry)

(revised)

25-MAR-2003 11-MAY-1998

AAW33395;

dd

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This protein sequence comprises human growth hormone receptor. The amino acid sequence was deduced from cDNA clones (see AAT94063) obtained from a human liver cDNA library, and shows 84% identity to the rabbit growth hormone receptor (see AAW33395). Human growth hormone receptor, its derivatives in which the cytoplasmic or transmembrane domains are deleted, and growth hormone binding proteins comprising amino acids 190-246 or 1-324 of the mature protein, can be used to treat disorders associated with growth hormone over-expression, e.g. gigantism and acromegally. The binding protein may also be used to increase the stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human and rabbit growth hormone receptor protein - useful to treat disorders associated with overexpression, e.g. gigantism and acromegaly.
                                                                                                                                                                                                                                                                                                                                                                   Growth hormone receptor; growth hromone binding protein; somatotropin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "translated codon is Ser in clone ghr.210 and ghr.110, Ile in ghr.501"
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                                                                                                                                                                                                                                                                                                                                                                                              human; gigantism; acromegaly; therapy
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                                                                                                                                                                                                                                                                                                                          Human growth hormone receptor.
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                          247. .269
  DDSWVEFIELDI 12
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HAMMONDS R G.
WOOD W I.
COLOSI P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-008010/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                    25-MAR-2003
11-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUN-1991;
08-JAN-1993;
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                                           339
                                                                                                                                                                                                           AAW33394;
Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LEUN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAMM/)
(WOOD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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                                                                                                                                         AAW33394
                                                                                                               RESULT
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This protein sequence comprises rabbit growth hormone receptor. The amino acid sequence was deduced from cDNA clones (see AAT94064) obtained from a rabbit liver cDNA library, and shows 84% identify to the human growth hormone receptor (see AAN3394). Rabbit and human growth hormone receptors, their derivatives in which the cytoplasmic or transmembrane domains are deleted, and growth hormone binding proteins comprising amino acids 190-246 or 1-324 of the mature proteins, can be used to treat disorders associated with growth hormone over-expression, e.g. gigantism and acromegaly. The binding protein may also be used to increase the stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                  note= "translated codon is Ala in clone ghr.435, Thr in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human and rabbit growth hormone receptor protein - useful to treat disorders associated with overexpression, e.g. gigantism and acromegaly.
                                                                                            Growth hormone receptor; growth hromone binding protein; somatotropin; rabbit; gigantism; acromegaly; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood
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                                                                                                                                                                                                                                             247. .269
/note= "transmembrane domain"
                                                                                                                                                                          1. .18
/label= Sig_peptide
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leung DW,
                                                                  Rabbit growth hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 8b; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                               87US-00062542.
91US-00723358.
93US-00002489.
                                                                                                                                                                                                                                                                                                                                       94US-00248B32
                                                                                                                                                                                                                               ghr.440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colosi PC, Spencer SA,
                                                                                                                                    Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                   LEUNG D W.
HAMMONDS R G.
WOOD W I.
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N-PSDB; AAT94064.
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                                                                                                                                                                                                    Misc-difference
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08-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                   (LEUN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (COLO/)
                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                             Domain
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Length 638;

Score 65; DB 2; Pred. No. 0.031;

100.0%;

Query Match Best Local Similarity

0

Gaps . 0

100.0%; Score 65; DB 2; Length 638; ilarity 100.0%; Pred. No. 0.031; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 12; Conserv

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Sequence 638 AA;
                                                                                                                                                                  Matches
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    SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein P16310, SEQ ID NO 10493
                                                                                                                                                                                                                                                                                                                                                                                   ADD45061 standard; protein; 638 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                          339 DDSWVEFIELDI 350
                 Conservative
                                                                                             1 DDSWVEFIELDI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER AG.
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                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD45061;
                     Matches
                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                            ADD45061
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ftp.wipo.int/pub/published pct sequences.

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comprising the vector. Among the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cubjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a contivity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that requires its activity is useful for preparing a medicament for ireating pain and a pharmaceutical composition comprising the one or more polymers is sectivity is useful for preparing a medicament for treating compliant (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene continued is a human protein (shown in Table 2 of therapy). The sequence presented is a human protein (shown in Table 2 of
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                               Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                            .;
0
100.0%; Score 65; DB 7; Length 638; 100.0%; Pred. No. 0.031; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Costigan M;
                                                                                                                                                                                                                                                                                                                                                   Human Protein P10912, SEQ ID NO 10499.
                                                                                                                                                                                                                              ADD45067 standard; protein; 638 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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                                                                                                                         340 DDŚWVEFIELDI 351
                                                  Conservative
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GENBANK; P10912.
                           Local Similarity
les 12; Conserv
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          Query Match
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the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                  100.0%; Score 65; DB 7; Length 638; 100.0%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                       Mismatches
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                     Local Similarity
es 12; Conserv
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                                                                                                                                                      Sequence 638 AA;
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                                                                                                                                                                                                                                                                           Matches
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pain and a pharmaceutical composition comprising the one or more

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, and enrivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal complexed to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a
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polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic construction injury (CI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                        Score 65; DB 7; Length 638; Pred. No. 0.031;
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                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat Protein P16310, SEQ ID NO 10497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD45065 standard; protein; 638 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 339 DDSWVEFIELDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woolf C, D'urso D,
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                 Sequence 638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENBANK; P16310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD45065;
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD45065
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Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
activity in an animal of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; dutg screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosolerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                     100.0%; Score 65; DB 7; Length 638; 100.0%; Pred. No. 0.031; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human growth hormone receptor homologue, SEQ ID NO:1807.
                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB11437 standard; peptide; 648 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-00496914.
2000US-00560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US003800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          340 DDSWVEFIELDI 351
                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 1 DDSWVEFIELDI 12
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-457740,
N-PSDB; ABA08681
                                                                                                                                                                                                                                                                      Sequence 638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157188-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB11437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
ABB11437
                                                                                                                                                                                                                                                                                                                                            Matches
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Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis

Claim 20; Page 189-190; 1963pp; English.

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contribution also relates to vectors and recombinant most centry of uncleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which colypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention activities; atem cell growth cactivity; and hence of inferentiation activities; stem cell growth activity; and including cytokine, cell proliferation or cell differentiation activity; activit, or inhibin-related activities; concentration or metastasis.

Concentration activities; receptor or ligand activities; or may be involved in oncogeneais, cancer cell proliferation or metastasis.

Conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell cancers), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial isohemana, bone disorders (e.g., osteoporosis), while those with conditions and useful or nucleic acids encoding them) may be used to promote wound certain and fungal infections in addition to immune disorders.

Competerial and fungal infections in addition to immune disorders or promote cell growth. For example, such polypeptides may be used to promote cell growth. For example, such polypeptides and nucleic each summent or replace cells encoding the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention
Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somatotropin receptor; SR; somatotropin binding protein; SBP; pRAT7-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serum somatotropin receptor protein from clone pRAT7-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 65; DB 4; L
100.0%; Pred. No. 0.031;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . . . 17
/label= signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR06473 standard; protein; 638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DDSWVEFIELDI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2003
04-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pRAT1-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Homology comparison between this putative rat somatotropin receptor and the published sequence indicates 70% identity. See also AAQ05689-91, AAQ06124 and AAQ05700. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is a polypeptide from the chicken growth hormone receptor. Sequences (AAY32794-Y32823) are examples of polypeptide sequences found at or near the ubiquitin/proteosome complex binding site located on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal transduction; proteolytic cleavage; growth hormone receptor; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
                                                                                                                                                                                                              Somatotropin binding protein and gene - used to regulate and/or modify activity of somatotropin in humans and animals.
                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 2; Length 638;
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken growth hormone receptor derived polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32794 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 9; 36pp; English.
                                                                                                                                                                                                                                                     Disclosure, Fig 6; 43pp; English.
                                                                 90EP-00102552
                                                                                           89US-00310725
                                                                                                                   (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                             93.8%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  340 DESWVEFIELDI 351
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                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               1 DDSWVEFIELDI 12
                                                                                                                                               Baumbach WR
                                                                                                                                                                        WPI; 1990-255493/34.
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                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                   N-PSDB; AAQ05691
                                                                                                                                                                                                                                                                                                                                   Sequence 638 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus
                                                                 09-FEB-1990;
                                                                                         17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1998;
                                       22-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-1999,
            EP383205-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP943624-A1
                                                                                                                                              Logan JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32794;
                                                                                                                                                                                                                                                                                                                                                             Query Match
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intracellular part of a cell surface receptor. These sequences are used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The inhibitor is either derived from, competes which might be present. The inhibitor is either derived from, competes which aight be present. The inhibitor is either derived from, and yary 32794-73823 are examples. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease
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Search completed: June 9, 2004, 15:48:26

Job time : 62 secs

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Gaps .. 0

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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model wa garian - protein search, protein

9, 2004, 15:43:40 ; Search time 13.2973 Seconds (without alignments) 86.807 Million cell updates/sec June Run on:

1 DDSWVEFIELDI 12 US-09-660-302D-2 65 score: Sequence: Title: Perfect :

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rec	somatotropin recep	somatotropin recep	somatotropin recep		1	somatotropin recep	arylphorin precurs	hypothetical prote	storage protein 2	vascular endotheli	hypothetical prote	protein-tyrosine k	transcription regu	transcription regu	signal recognition	hypothetical prote	probable 3-oxoacyl	_		_	ਰ			6-C	probable RNA helic	probable helicase	reelin precursor -	heparan sulfate pr
SUMMARIES	qi	833339	A33505	A33991	B28176	S12136	833608	S32823	A61619	866916	A34287	JC4954	AD2113	I58375	AF1115	AG1476	T03951	AG2426	E70027	7192	B64589	T19514	G83112	875238	T27468	S00742	G91286	8612	588	825
	DB	. 2	7	7	7	Ŋ	7	7	N	N	~	~	~	~	~	ď	7	7	٦	7	7	~	N	7	~	Н	7	~	7	7
	Length	634	638	638	638	638	677	608	702	411	704	1379	442	1363	300	300	103	217	264	321	321	829	1399	363	489	698	2113	2113	3461	3707
dł	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	8.06	73.8	66.2	66.2	63.1	61.5	61.5	60.8	60.8	0.09	60.0	0	0	60.0	0	ö	58.5	8	œ	8	œ	œ.	7.
	Score	65	65	65	65	65	65	59	48	43		41	40	40	39.5	6.	39	39	39	39	39	39	39	38	38		38	38	m	37.5
	Result No.		7	е	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29

perlecan precursor 5-methylcytosine-s	conserved hypothet	hypothetical prote	exonuclease 47 (EC	hypothetical prote	conserved hypothet	F16N3.15 [imported	hypothetical prote	hypothetical prote	segment S5 protein	probable large ATP	spalt-related prot	protein-tyrosine k	MATal splicing fac	probable membrane
A38096 AT3299	E70357	S74631	NCBPX4	D64028	G69341	C96516	AF2097	T09036	A39972	T36175	T13805	A48999	S18510	261667
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01 00	~	N	_		•		•	•	•					
4391 2	198 2	258 2	339	436	457	473	595	648	804	840	1263	1298	355	1107
57.7 4391 2	56.9 198 2					56.9 473			56.9 804		56.9 1263	_		_
37.5 57.7 4391 2 37 56.9 190 2		56.9		56.9							• •	_		_

AL I GNMENTS

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Nilternate names: growth hormone receptor
Cispeciaes: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispeciaes: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispeciaes: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispeciaes: Ovis orientalis aries, Ovis ammon orientalis orientalis aries, Ovis ammon orientalis arequence_revision orientalis arequence_revision orientalis area orientalis orientalis orientalis area orientalis area orientalis area orientalis orientalis orientalis orientalis area orientalis o
somatotropin receptor - sheep
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. 0 Gaps ·, Score 65; DB 2; Length 634; Pred. No. 0.0037; ; Mismatches 0; Indels 0; 100.0%; larity 100.0%; Conservative 0 Query Match Best Local Similarity Matches 12; Conserv

DDSWVEFIELDI 346 1 DDSWVEFIELDI 12 335 g ò

RESULT 2

A33505

somatotropin receptor precursor - rac
N; Alternate names: growth hormone receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 02-Au
C; Accession: A32985; A33505 _
R; Baumbach, W.R.; Horner, D.L.; Logan, J.S.
Genes Dev. 3, 1199-1205, 1989
A; Title: The growth hormone-binding protein in rat serum is an alterr
A; Reference number: A32985; MUID: 90006741; PMID: 2792761
A;Accession: A32985

natively spliced for

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: GB:X16726
R;Mathews, L.S.; Enberg, B.; Norstedt, G.
R;Mathews, L.S.; Enberg, B.; Norstedt, G.
A;Title: Regulation of rat growth hormone receptor gene expression.
A;Reference number: A33505; MUID:89255563; PMID:2722883
A;Accession: A33505
A;Accession: A33505
A;Accession: A33505
A;Accession: A33505
A;Accession: A33505
A;Cross-references: GB:U04811; NID:g204308; PIDN:AAA41219.1; PID:g204309
A;Cross-references: GB:U04811; NID:g204309;

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339 DDSWVEFIELDI 350
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-638 <CIO>
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                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: growth hormone receptor
N; Contains: somatotropin-binding protein, serum
C; Species: Homo sapiens (man)
C; Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 02-Aug-2002
C; Accession: A33991; S04530
C; Accession: A33991; S04530
C; Accession: A33991; S04530
Marchan, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; Rd Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989
A; Title: Characterization of the human growth hormone receptor gene and demonstration of A; Reference number: A33991; MUID:90046742; PMID:2813379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-638 <GOD>
A;Residues: 1-638 <GOD>
A;Residues: 1-638 <GOD>
A;Residues: GB:MZ8458; GB:MZ8459; GB:MZ8460; GB:MZ8461; GB:MZ8462; GB:NZ8463; GB
A;Cross-references: GB:MZ8458; GB:MZ8459; GB:MZ8460; GB:MZ8461; GB:MZ8462; GB:MZ8463; GB
B;Cross-references: GB:MZ8458; GB:MZ8459; GB:MZ8460; GB:MZ8461; GB:MZ8462; GB:MZ8463; GB:MZ84530; MUID:88065896; PMID:Z825030
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NyAlternate names growth hormone receptor
NyAlternate names growth hormone receptor
NyContains: somatotropin-binding protein, serum
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1990 #sequence revision 10-Mar-1994 #text_change 02-Aug-2002
C;Accession: 808544; B28176; $\bar{A}28176$
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;
Nature 330, 537-543, 1987
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A;Reference number: S04530; MUID:88065896; PMID:2825030
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology C;Keywords: transmembrane protein
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C,Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C,Keywords: liver; transmembrane protein
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A;Cross-references: GB:AF015252; NID:g2342651; PIDN:AAB67613.1; PID:g2342652
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                                                                                                                                                      Gaps
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A;Residues: 1-543,'1',545-638 <LEU>
A;Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738
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                                                                                           Length 638;
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                                                             Score 65; DB 2; Length 630
Pred. No. 0.0037;
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                                                                                        100.0%;
100.0%;
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Best Local Similarity 100."
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                                                                               Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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A;Note: part of this sequence, including the amino end of the mature protein, was configurable to the mature protein, was configurable to them. 263, 7862-7867, 1988
A;Title: Rabbit liver growth hormone receptor and serum binding protein. Purification, A;Reference number: A92721; MUID:88227992; PMID:3372509
A;Accession: B28176
A;Molecule type: protein
A;Residues: 19-34;SPG', 81-88;X',99,'XX',102-105,'X',107-110,'XX',113-114;'X',141,'X', -57-6-77;59-595 <8Ps>
A;Note: sequence is derived from intact receptor
A;Note: sequence is derived from intact receptor
A;Note: sequence is derived from a soluble form of the receptor isolated from serum
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology C;Reywords: glycoprotein; liver; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>F;10-68/Domain: transmembrane #status experimental <AMT>
F;265-288/Domain: transmembrane #status predicted <TAMN>
F;46,200/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C'Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Aug-2002
C'Accession: 533608; 533607
C'Accession: 533608; 533607; MulD:89295449; PMID:2739661
A;Title: Mouse serum growth hormone (GH) binding protein has GH receptor extracellular A;Reference number: 533607; MulD:89295449; PMID:2739661
A,Recession: 533608
A,Molecule type: mRNA
A,Residues: 1-677 <SMI>A;Cross-references: EMBL:M3324; NID:g193508; PIDN:AAA37690.1; PID:g309253
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C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein
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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S1213 # Wang, X.; Kopchick, J.J.
Nucleic Acids Res. 18, 6451, 1990
A;Title: Porcine growth hormone receptor CDNA sequence.
A;Reference number: S12136; MUID:91057155; PMID:2243805
A;Accession: S12136
A;Accession: S12136
A;Accession: Lype: mRNA
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Best Local Similarity 100..
Thes 12; Conservative
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Query Match

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A.Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellonel A, Reference number: A61619
A, Accession: A61619
A, Accession: A61619
A, Molecule type: DNA
A, Residues: 1-702 < AREM>
A, Residues: 1-702 < AREM>
A, Residues: 1-702 < AREM>
A, Residues: 1 & PID: G159078
A, Note: in the authors' translation, residue 306-Leu is omitted, residue 317-Asn is dupl C, Genetics: 30/1; 74/3; 352/3; 410/2
A, Note: single copy gene
C, Genetics: single copy gene
C, Genetics: single sopy gene
C, Geyperfamily: arylphorin
C; Keyperfamily: arylphorin
C; Keyperfamily: arylphorin
C; Keyperfamily: singlal sequence #status predicted <SIG>
F;1-16/Domain: signal sequence #status predicted <SIG>
F;211, 481/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.
Biol. Chem. 264, 11020-11025; 1989
A;Title: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mq
A;Reference number: A34287; MUID:89291839; PMID:2544581
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A;Molecule type: DNA
A;Residues: 1-411 <LAN>
A;Cross-references: EMBL:Z74949; NID:g1420165; PID:e251966; PID:g1420167; GSPDB:GN00015;
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NyAlternate names: hypothetical protein 02762
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 12-Uul-1996 #sequence_revision 12-Uul-1996 #text_change 19-Apr-2002
C;Accession: S66916
R;Landt, O.; Hiesell, R; Unseld, M.
Bibmitted to the Protein Sequence Database, July 1996
A;Reference number: S66907
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C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 04-Sep-1998
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Pred. No. 12;
4; Mismatches 2; Indels
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4; Mismatches
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50.0%;
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ilarity 54.5%;
Conservative
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A;Gene: MIRS:YOR042w
A;Cross-references: SGD:S0005568
A;Map position: 15R
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546 EDNWINFIELD 556
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C,Superfamily: arylphorin
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Best Local Similarity
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S66916
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R; Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.
Mol. Endocrinol. 7, 1391-1398, 1993
A; Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf c A; Reference number: A49812; MUID:94158898; PMID:8114754
A; Accession: A49812
A; Status: preliminary
A; Molecule type: mRNA
A; Rose-references: G8:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138
A; Experimental source: liver, normal chicken
A; Experimental source: liver, normal chicken
C; Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C; Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane proteil
F; 1-22/Domain: signal sequence #status predicted csign.
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                    A, Experimental source: liver
A, Accession: S33607
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule: 1-324 < kSM2>
A, Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252
C, Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C, Keywords: glycoprotein; receptor; transmembrane protein
F;1-18/Domain: signal sequence #status predicted < SIG>
F;19-677/Product: somatotropin-binding protein, high molecular weight #status predicted
F;274-297/Domain: transmembrane #status predicted < TMM>
F;40,164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted
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NiAlfernate names: phenylalanine-rich protein Lhp76
CiSpecies: Galleria mellonella (greater wax moth)
CiSpecies: 21-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999
CiAccession. A61619
Rimemel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 333-342, 1992
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Matches 12; Conservative
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A;Residues: 1-608 <BUR>
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RESULT 8 A61619

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transcription regulators homolog lmo0325 [imported] - Listeria monocytogenes (strain EG
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001
C;Dominguez-Bernal, G;Duchaud, E;Durand, L;Dussurget, O;Entian, K.D.;Fsihi, H.D.;Jones, L.M;Karst, U.
C;Dominguez-Bernal, G;Duchaud, E;Durand, L;Dussurget, O;Entian, K.D.;Fsihi, H.D.;Jones, L.M;Karst, U.
C;Conece 294
A;Authors: Kreft, J;Kuhn, M;Kunst, F;Kurapkat, G;Madueno, E;Maitournam, A;Mok, C;Schlueter, T;Simoes, N;Tierrez, A;Vazquez-Boland, J.A.;Voss, H;Wehland, A;Reference number: ABI077;MUID:21537279;PMID:11679669
A;Accession: AFI15
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1476
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
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63.6%; Pred. No. 34;
ive 3; Mismatches 0;
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75.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                    C;Accession: JC4954
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor A;Reference number: JC4953; MUID:97017121; PMID:8863722
A;Accession: JC4954
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-1379 <EIC.
C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology (K)-20/Domain: signal sequence #status predicted <IGNO
F;1-20/Domain: signal sequence #status predicted <IGNO
F;789-810/Domain: protein kinase homology <KIN>
F;864-872/Region: protein kinase AlP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AD2113
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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A;Cross-references: GB:BA000019; PIDN:BAB74158.1; PID:g17131551; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                         vascular endothelial growth factor receptor 2 precursor - Japanese quail NiAlternate names: Quail endothelial kinase 2; Quek 2 (Species: Coturnix coturnix japonica (Japanese quail) C.Species: Coturnix coturnix japonica (Japanese quail) C.Species: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999
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C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Feb-2000
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2; Mismatches
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Pred. No.
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60.0%;
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EDNWMKFFELD 553
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Matches 6; Conserv
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Matches 6; Conserv
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A;Gene: all2459
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Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-8852, 200.

Science 294, 849-8852, 200.

Science 294, 849-8852, 200.

Schout S.; Kubn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Helerance number: AB1077; MUID:21537279; PMID:11679669

A.; Reference number: AB1077; MUID:21537279; PMID:11679669

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A.; Residues: 1-300 ocid.A.

A.; Residues: 1-300 ocid.A.

A.; Experimental source: strain Clip11262

C.; Genetics:

A.; Genetics:

A.
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Gaps 1; Query Match
60.8%; Score 39.5; DB 2; Length 300;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 0; Indels 1

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1 DDS-WVEFIEL 10

73 DDSFWIDFVEL 83

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Search completed: June 9, 2004, 15:52:16 Job time: 14.2973 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2004, 15:36:55; Search time 8.75676 Seconds (without alignments) 71.355 Million cell updates/sec June on: Run

US-09-660-302D-2 65 Perfect score:

1 DDSWVEFIELDI 12

Sequence:

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Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

141681 seqs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ø	Description	P79108 bos taurus	5 ovi	homo	macac	P19756 sus scrofa	P19941 oryctolagus			Q02092 gallus gall	Q90375 columba liv		. ,		P35917 mus musculu		Q9hwc9 pseudomonas	P11947 tetrahymena	P78509 homo sapien	-	P58751 rattus norv	Q05793 mus musculu	P98160 homo sapien				P44183 haemophilus	P12366 wound tumor	P35916 homo sapien	32357	P05071 tobacco rat	4451	O29556 archaeoglob	9278
SUMMARIES	ID	GHR BOVIN	GHR SHEEP	GHR HUMAN	GHR MACMU	GHR PIG	GHR RABIT	GHR RAT	GHR MOUSE	GHR CHICK	GHR COLLI	RPOC PSEPU	SSP2 BOMMO	Y4FP RHISN		SR09 MAIZE	RPOC PSEAE	COX1 TETPY	RELN HUMAN	RELN MOUSE	RELN RAT	PGBM_MOUSE	PGBM HUMAN	GLBC_NIPBR	EXO1 BPT4	MURB SHEON	YE09 HAEIN	VPS WTV	VGR3 HUMAN	AAR2 YEAST	COAT TRVPS	YOEF BACSU	THI4 ARCFU	YQIS_CABEL
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P53687 saccharomyc	P74360 synechocyst	P45942 bacillus su	Q08908 saccharomyc	Q00468 candida mal	P24131 clostridium	P38114 saccharomyc	P39770 drosophila	P39806 drosophila	032202 bacillus su	Q58018 methanococc	P41302 photobacter
HST3_YEAST	YF26 SYNY3	YOCG_BACSU	FRE5 YEAST	CAO2 CANMA	BGAL_CLOAB	YB00 YEAST	SALM_DROME	SALM DROVI	YVQI BACSU	THI4 METJA	LUXD_PHOPO
ч	Н	н	Н	Н	Н	н	Н	Н	-1	-4	Н
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55.4	55.4	55.4	55.4	55.4	55.4	55.4	55.4	55.4	53.8	53.8	53.8
36	36	36	36	36	36	36	36	36	35	32	35

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. .) (POTENTIAL) (GLCNAC. .) (POTENTIAL) (GLCNAC. .) (POTENTIAL)
                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELULAR (POTENTIAL).

EXTRACELULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X70041; CAA49635.1; -.
HSSP; P10912; 1A22.
InterPro; IPR003296; CR1A.
InterPro; IPR003296; FN1II.
InterPro; IPR003528; Hemtopoptn_LF1.
Pfam; PF00041; fn3; 1.
PROSITE; PS01352; HEMATOPO REC_LF1; 1.
PROSITE; PS01352; HEMATOPO REC_LF1; 1.
Receptor; Transembrane; Glycoprotein; Signal.
SIGNAL
  634 AA.
PRT;
STANDARD;
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284
634
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66
108
136
46
73
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NCBI_TaxID=9913;
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GHR.
GHR BOVIN
P79108;
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                                                                                                                                                                                                                                                                                                                                                   Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
"The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expression in the liver."
MOI. Cell. Endocrinol. 73:135-145(1990).
-!- FUNCTION: This is a receptor for pituitary gland growth hormone.
-!- SUBUNIT: Homodiamer (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                           Gaps
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY CHILLARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
           (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                           0;
                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                     Length 634;
                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GROWTH HORMONE RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Subfamily 1.
                                 91955A28296CBD2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                     100.0%; Score 65; DB 1; I
100.0%; Pred. No. 0.00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P10912, 1AXI.
InterPro; IPR001296; CRIA.
InterPro; IPR0013961; FN III.
InterPro; IPR0013961; FN III.
InterPro; IPR0013528; Hemtopoptn_L_F1.
Pfam; PF00041; fn3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                       634 AA.
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                       PRT;
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                                 70979 MW;
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                                                                                                             335 DDSWVEFIELDI 346
                                                                           12; Conservative
                                                                                               1 DDSWVEFIELDI 12
                                                                                                                                                                       STANDARD;
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                                 634 AA;
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9940;
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Q28575;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       demonstration of a partial gene deletion in two patients with Laron-type dwarfism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R.,
Keret R., Rotwein P.S., Parks J.S., Laron Z., Wood W.I.;
"Characterization of the human growth hormone receptor gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C., Henzel W.J., Barnard R., Waters M.J., Wood W.I.; "Growth hormone receptor and serum binding protein: purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                -LINKED (GLCNAC. ..) (POTENTIAL)
-LINKED (GLCNAC. ..) (POTENTIAL)
-LINKED (GLCNAC. ..) (POTENTIAL)
FPD28B9C23EC1496 CRC64;
     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 13, Last amnotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93278381; PubMed=8504296;
Amselem S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,
Valleix S., Goossens M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Spectrum of growth hormone receptor mutations and associated haplotypes in Laron syndrome."; Hum. Mol. Genet. 2:355-359(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fuh G., Mulkerrin M.G., Bass S., McFarland N., Brochier M., Bourrel J.H., Light D.R., Wells J.A.; The human growth hormone receptor. Secretion from Escherich and disulfide bonding pattern of the extracellular binding J. Biol. Chem. 265:3111-3115(1990).
                                                                                                                                                                           Length 634;
                                                                                                                                                                                                                                0; Indels
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                         Score 65; DB 1; I
Pred. No. 0.00069;
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Mismatches
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MEDLINE=94185645; PubMed=8137822;
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                                                                                                                       70844 MW;
                                                                                                                                                                                                                                                                                                                                               335 DDSWVEFIELDI 346
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                                                                                                                                                                                                         Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                       1 DDSWVEFIELDI 12
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634 AA;
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M28461, AAA52555.1; JOINED.
M28462; AAA52555.1; JOINED.
M28463; AAA52555.1; JOINED.
M28464; AAA52555.1; JOINED.
M28465; AAA52555.1; JOINED.
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                                                                      PIR, A33911, A33911.
PDB, 3HHR, 30-APR-94.
PDB, 1HWG, 19-NOV-97.
PDB, 1HWH, 19-NOV-97.
PDB, 1AXI; 28-JAN-98.
PDB, 1AXI; 29-APR-98.
PDB, 1KF9; 20-NOV-02.
Genew, HGNC:4263; GHR.
                                                                                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 1.
SMART; SM00060: FM3: 1.
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EMBL;
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                                                           EMBL;
PIR;
PDB;
   DONA NA PRINTINA NA PERINTINA NA
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                                                                                                                                                   MEDLINE=96013502; PubMed=7565946; Goddard A.D., Covello R., Luoh S.-M., Clackson T., Attie K.M., Goddard A.D., Covello R., Luoh S.-M., Carlsson L.M.S.; Gesundheit N., Rundle A.C., Wells J.A., Carlsson L.M.S.; "Mutations of the growth hormone receptor in children with idiopathic short stature.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579. MEDLINE=99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure of an antagonist mutant of human growth hormone, G120R, in complex with its receptor at 2.9-A resolution."; J. Biol. Chem. 271:32197-32203(1996).
   Dusquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R., Savage M.O., Preece M.A., Craescu C.T., Blouquit Y., Goossens M.,
                                           "A single amino acid substitution in the exoplasmic domain of the human growth hormone (GH) receptor confers familial GH resistance (Laron syndrome) with positive GH-binding activity by abolishing receptor homodimerization.";
EMBO J. 13:1386-1395(1994).
                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.
MEDLINE=97113023; PubMed=8943276;
Sundstroem M., Lundqvist T., Roedin J., Glebel L.B., Milligan D.,
                                                                                                                                                                                                                                                                      MEDLINE=92196577; PubMed=1549776; de Vos A.M., Ultsch M., Kossiakoff A.A.; "Human growth hormone and extracellular domain of its receptor: crystal structure of the complex."; Science 255:306-312(1992).
                                                                                                                                      VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-256.
                                                                                                                                                                                                                            New Engl. J. Med. 333:1093-1098(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X06562; CAA29808.1; -.
EMBL, M28466; AAA52555.1; -.
BMBL, M28458; AAA52555.1; JOINED.
EMBL, M28459; AAA52555.1; JOINED.
EMBL, M28460; AAA52555.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23:373-373 (1999)
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Lander E.S.

ERRATUM

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D -> H (in Laron dwarfism, abolish receptor homodimerization).
Fride-vap 002713.
R -> C (in Laron dwarfism and idiopathic short stature).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> H (in dbSNP:6177).
FFIGE-VAR 0.1939a.
S -> D (in idiopathic short stature)
FFIGE-VAR_002716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E -> K (in idiopathic short stature)
/FTId=VAR 002708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                           PROSITE; PS01352; HEMATOPO REC L F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure; Dwarfism; Polymorphism; Disease mutation.

1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 1; Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R -> K (in Laron dwarfism).
/FTIG=VAR 002709.
F -> S (in Laron dwarfism).
/FTIG=VAR 002710.
V -> A (in Laron dwarfism).
/FTIG=VAR 002711.
/FTIG=VAR 002712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_002714.

R -> H (in dbSRP:6181).
/FTId=VAR_013937.

FTId=VAR_013937.
/FTId=VAR_002715.
GO; GO:0005887; C:integral to plasma membrane; TAS: GO; GO:0004903; F:growth hormone receptor activity; TAS: GO; GO:0007150; P:growth pattern; TAS: GO; GO:0001510; P:growth patern; TAS: GO; GO:0001501; P:skeletal development; TAS.
                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                               GROWTH HORMONE RECEPTOR
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P -> T (in dbSNP:6183)
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FTId=VAR
                                                                                                InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_F1.
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Matches
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97373601; PubMed=9228076;
Martini J.F., Pezet A., Guezennec C.Y., Edery M., Postel-Vinay M.C.,
Kelly P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Monkey growth hormone (GH) receptor gene expression. Evidence for two mechanisms for the generation of the GH binding protein.";
J. Biol. Chem. 272:18951-18958 (1997).
-!- FUNCTION: This is a receptor for pituitary gland growth hormone.
-!- SUBCURIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                 ·,
                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                              Indels
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CYTOPLASMIC (POTENTIAL).
FIBRONSCTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
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100.0%; Pred. No. 0.0007;
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Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL 18
                                                                                                                                                                                                                                                                                                                                       638 AA.
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InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_F1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
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HSSP; P10912; 1AXI.
                                                                                                                                                                              339 DDSWVEFIELDI 350
                                                              12; Conservative
                                                                                                                      1 DDSWVEFIELDI 12
                                                                                                                                                                                                                                                                                                                                    STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=Landrace-Yorkshire, TISSUE=Liver;
MEDLINE=91057155; PubMed=2243805;
Cioffi J.A., Wang X., Kopchick J.J.;
"Porcine growth hormone receptor cDNA sequence.";
Nucleic Acids Res. 18:6451-6451(1990).
                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer.
-!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 1.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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(POTENTIAL).
                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
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FIBROMECTIN TYPE-III.
BY SIMILARITY.
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N-LINKED (GLCNAC...) (P.
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SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO REC L F1; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
  638 AA.
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PIR; $12136; $12136.
HSSP; P10912; 1A22.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_FI.
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                                                                                                        Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                 MEDLINE=90006741; PubMed=2792761;

Baumbach W.R., Horner D.L., Logan J.S.;

"The growth hormone-binding protein in rat serum is an alternatively spliced form of the rat growth hormone receptor.";

Genes Dev. 3:1199-1205(1989).

-!-FRUCTION: This is a receptor for pituitary gland growth hormone.
           P16310;
01-MUG-1990 (Rel. 15, Created)
01-MUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=89255563; PubMed=2722883;
Mathews L.S., Enberg B., Norstedt G.;
Megulation of tra growth hormone receptor gene expression.";
J. Biol. Chem. 264:9905-9910(1989).
                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of
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HSSP; PIO121; LAZ2.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_LFI.
Pfan; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
Receptor; Transmembrane; Glycoprotein; Signal.
SIGNAL
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily II.
-:- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                         Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C., Henzel W.J., Barnard R., Waters M.J., Wood W.I.; Growth hormone receptor and serum binding protein: purification, cloning and expression.";
Nature 330:537-543(1987)."
                                                                                                                                        Eukaryotā; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                       01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
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FIBRONECTIN TYPE-III.
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InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN III.
InterPro; IPR003529; Hemtopoptn_L.F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO REC_L.F1; 1.
SIGNAL 1 18
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MEDLINE=88065896; PubMed=2825030;
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                                       (Rel. 17, Created)
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Matches 12; Conservative
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GHR RAT RESULT

EXTRACELLULAR (POTENTIAL) POTENTIAL.

CYTOPLASMIC (POTENTIAL) FIBRONECTIN TYPE-III.

GROWTH HORMONE RECEPTOR

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                                                                                                                                                                                                                                                    [2] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). STRAIN-Swiss Webster, and DBA/2J;
MEDLINE=99367316; PubMed=10425445;
Moffat J.G., Edens A., Talamantes F.;
"Structure and expression of the mouse growth hormone receptor/growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormone receptor.";
Mol. Endocrinol. 2:108-116(1988).

-!- FUNCTION: Isoform 1 is a receptor for pituitary gland growth hormone. Isoform 2 is a serum growth hormone binding protein that may play an important role in regulating the effective serum concentration of gh.

-!- SUBUNIT: Isoform 1 is a homodimer.

-!- SUBUNIT: Isoform 1.
             CHR. MOUSE

ID GHR MOUSE

ID 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last sequence)

DF Growth hormone receptor precursor (GH receptor) (GH binding protein)

DE (GHBP) (Serum binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou Y., He L., Kopchick J.J.;
"An exon encoding the mouse growth hormone binding protein (mGHBP) carboxy terminus is located between exon 7 and 8 of the mouse growth hormone receptor gene."

Receptor 4:223-227(1994).
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=Swiss Webster, and DBA/2J;
MEDLINE=95080157; PubMed=7988474;
Bdens A., Southard J.N., Tamantes F.;
"Mouse growth hormone receptor/binding protein and growth hormone receptor from a single gene by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isola=p16882-1; Sequence=Displayed;
Name=2; Synonyms=LMW GHR;
Isold=P16882-2; Sequence=VSP_001716, VSP_001717;
SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-89295449; PubMed=2739661;
Smitch W.C., Kuniyoshi J., Talamantes F.;
Whouse serum growth hormone (GH) binding protein has GH receptor extracellular and substituted transmembrane domains.";
Mol. Endocrinol. 3:984-990(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE=88288223; PubMed=3398846;
Smith W.C., Colosi P., Talamantes F.;
"Isolation of two molecular weight variants of the mouse growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou Y., He L., Kopchick J.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
Event=Alternative splicing, Named isoforms=2,
Name=1; Synonyms=HMW GHR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Endocrinology 135:2802-2805(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95201642; PubMed=7894338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 25-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6
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       RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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FIDNHLYHQLQRIRH (in isoform 2).

FTIG=VSP 001716.

Missing (in isoform 2).

FTIG=VSP 001717.

T -> A (IN REF. 6).

G -> A (IN REF. 2).

E -> G (IN REF. 2).
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Subfamily 1. SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95653380CAF0B931 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH HORMONE RECEPTOR
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InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_F1.
SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                           AF120486; AAD32556.1; JOINED.
AF120487; AAD32556.1; JOINED.
AF120488; AAD32556.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                   AF120487, AAD32555.1; -.
AF120481, AAD32555.1; JOINED.
AF120482, AAD32555.1; JOINED.
AF120483, AAD32555.1; JOINED.
                                                                                                                                                                                                                          AF120489; AAD32556.1; --
AF120481; AAD32556.1; JOINED
AF120482; AAD32556.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF120484; AAD32555.1; JOINED
AF120485; AAD32555.1; JOINED
AF120486; AAD32555.1; JOINED
                                                                                                                                                                                                                                                                            AF120483; AAD32556.1; JOINED
                                                                                                                                                                                      EMBL; M31680; AAA37689.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U49268; AAK62802.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U43933; AAK62802.1; JOINED P10912; 1A22.
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AAD32556.1;
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650 AA;
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12; Conser
                                                                                                                                                                                                                                                                                               AF120484;
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RESULT 10
                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                         Burnside J., Liou S.S., Cogburn L.A.,
"Molecular cloning of the chicken growth hormone receptor
complementary decoxyribonucleic acid: mutation of the gene in
sex-linked dwarf chickens.";
Endocrinology 128:3183-3192(1991).
--- FUNCTION: This is a receptor for pituitary gland growth hormone.
                                                                                                                                                                                                                                                                            -i- SUBUNIT: Homodimer.
-i- SUBCELULAR LOCATION: Type I membrane protein.
-i- TISSUB SPECIFICITY: Broad specificity.
-i- SIMILARITY: Belongs to the type I cytokine family of receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                  01-JUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.8%; Score 59; DB 1; Length 608;
                                                                                                                                                                                                                                                                                                                         Subfamily 1.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D71AD7B6C62528DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROWTH HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL) FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO REC_LF1; 1.
PROSITE; PS01352; HEMATOPO REC_LF1; 1.
SIGNAL
                     608 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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PIR; S32823; 332823.
HSSP, P10912; JAXI.
INTEFPCO, IPRO02996; CRIA.
INTEFPCO; IPRO08967; FN III-like.
INTEFPCO; IPRO03961; FN III-like.
INTEFPCO; IPRO03528; Hemtopoptn_LF1.
                                                                                                                                                                                                  MEDLINE=91243665; PubMed=2036984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68572 MW;
                                           (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duery Match
Bust Local Similarity 91.79,
Bust Local 11; Conservative
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
608
223
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83
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                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
17
238
262
117
                                                                                                                                                      NCBI_TaxID=9031;
                                           01-JUL-1993
                     GHR CHICK
Q02092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
                                                                                    protein).
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                                                                                                                                              Gallus
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RESULT 9
GHR_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheng C.H.K., Shaw P.C., Teim K.W.K., Lau K.F.;
Submitted (JAN-1996) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: This is a receptor for pituitary gland growth hormone.
-!- SUBDUIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(AAC...) (POTENT'
(POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Columba livia (Domestic pigeon).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba VCBI_TaxID=8932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·:
                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 611;
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EXTRACELLULAR (POTENTIAL).

COTOFLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POT N-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Subfamily 1.
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RINEEPRO; IPR00396; FN III-like.
R InterPro; IPR003961; FN III-like.
R InterPro; IPR003528; Hemtopoptn_LFI.
Fpan; PF00041; fn3; 1.
FR0317E; SM0060, FN3; 1.
FR051TE; PS01352; HEMATOPO_REC_LFI; 1.
FRC6EPLO; Transmembrane; Glycoprotein; Signal.
SIGNAL
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Pred. No. 0.0078;
); Mismatches 1
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                                         611 AA
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                                                                                                                                        (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 43, Last anno
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                                                                                                                                                  01-NOV-1997
GHR_COLLI
ID GHR_COLLI
AC Q90375;
                                                                                                                                                                                                                                                                                                                                                    protein).
GHR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESPUENCE OF 1-497 FROM N.A.

MEDLINE=89117617; PubMed=1219131;

MEDLINE=89117617; PubMed=1219131;

MEDLINE=89117617; PubMed=1219131;

MORDINE=89117617; PubMed=1219131;

MORDINE=89117617; PubMed=1219131;

MORDINE=89117617; PubMed=1219131;

MORDINE=89117617; PubMed=121913;

MORDINE=89117617;

MORDINE=12917;

MORDINE=89117617;

MORDINE=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Danilkovich A.V., Borodin A.M., Allikmets R.L., Rostapshov V.M.,
Chernov I.P., Azhikina T.L., Monastyrskaya G.S., Sverdlov E.D.;
"Nuclectide sequence of the rpoC gene coding for the beta'-subunit of
RNA polymerase in Pseudomonas putida.";
Dokl. Blochem. 303:241-245(1988).
                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substrates.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '{kNA}(N).
-!- SUBUNIT. The enzyme consists of the sigma chain and the core
enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
beta' chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription.
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                                          PRT; 1409 AA
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EMBL, M3819; AAA25987.1; --
PIR, JON420; UN0420.
HSSP: QSKWIG; 1HQM.
INTERPRO; IPR000722; RNA_POL_RPbl 1.
INTERPRO; IPR007080; RNA_POL_RPbl 1.
INTERPRO; IPR007080; RNA_POL_RPbl 1.
INTERPRO; IPR007081; RNA_POL_RPbl 4.
INTERPRO; IPR007081; RNA_POL_RPbl 4.
INTERPRO; IPR007081; RNA_POL_RPbl 5.
INTERPRO; IPR007081; RNA_POL_RPbl 6.
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Pfam, PF04983; RNA POL RPB1.; 1.
Pfam; PF04983; RNA POL RPB1.3; 1.
Pfam; PF05000; RNA POL RPB1.3; 1.
STAM; SNOW POL RPB1.4; 1.
SNART; SNOW POL RPB1.5; 1.
Transferase; DNA-directed RNA POlyme
                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas.
                                                                                                           (Rel. 16, Created)
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                              Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=303;
                                                                                                           01-NOV-1990
                              RPOC_PSEPU
P19176;
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   may serve as a store
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89291839; PubMed=2544581;
Fujii T., Sakurai H., Izumi S., Tomino S.;
"Structure of the gene for the arylphorin-type storage protein SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEX-SPECIAL.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

'Tranac. . . ) (POTENTIAL).
                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Bombyx mori.";

J. Biol. Chem. 264:11020-11025(1989).

-!- FUNCTION: Larval storage protein (LSP) which may serve a of amino acids for synthesis of adult proteins.

-!- SUBCELLULAR LOCATION: Extracellular.

-!- TISSUE SPECIFICITY: Fat body.

-!- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
                                                73.8%; Score 48; DB 1; Length 1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEX-SPECIFIC STORAGE-PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 704;
                                                                                Indels
                154544 MW; C5662109D3BE3D81 CRC64;
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                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                            704 AA
                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update
Sex-specific storage-protein 2 precursor.
                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB
Pred. No. 6.6;
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HSSP, P04253; 10XY.
INTERPO: IPR008922; Di-copper centre.
INTERPO: IPR00896; Hemocyanin.
INTERPO: IPR005203; hemocyanin.
INTERPO: IPR005204; hemocyanin.
INTERPO: IPR005204; hemocyanin.
France i PR005204; hemocyanin.
France i PR007110; Ig-like.
France i PR00713; hemocyanin.; I.
Pfam; PF03722; hemocyanin.; I.
                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Storage protein; Glycoprotein.
SIGNAL 16
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PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
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EMBL; M24371; AAA27848.1; JOINED.
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54.5%;
                                                            Local Similarity 72.7
les 8; Conservative
                                                                                                                                          876 DEOWVEFIELN 886
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                                                                                                                                                                                                                                                                                                                                   Bombyx mori (Silk moth)
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P20613;
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
(VEGFR-3) (Tyrosine-protein kinase receptor FLM4).
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:394-401(1997).
-!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable ABC transporter periplasmic binding protein Y4FP precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
-!- SIMILARITY: SOME, TO S.MARCESCENS IRON(III)-BINDING PERIPLASMIC
PROTEIN AND TO H.INFLUENSH PH0131.
-!- CAUTION: It is uncertain whether Met-1 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AEGUGUO,3; ARDJACI.
InterPro; JFROGGO59; SSP bac 1.
Pfam; PFG1547; SBP bac 1; 1.
Hypothetical protein; Transport; Periplasmic; Signal; Plasmid.
SIGNAL
46 OR 34, OR 40, OR 41 (POTENTIAL).
CHAIN 47 358 PROBABLE ABC TRANSPORTER PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobium/Agrobacterium group, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 40; DB 1; Length 358;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING PROTEIN Y4FP
  1;
                                                                                                                                                                                  358 AA.
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3; Mismatches
Mismatches
                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                            Rhizobium sp. (strain NGR234)
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Conservative
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                                                                              543 EDNWMKFFELD 553
                                                                                                                                                                                  STANDARD;
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                                        1 DDSWVEFIELD 11
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nes 7; Conserv
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P35917;
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1D VGR3 M
A D35917
DT 01-JUN
DT 10-CT
DE VEGFR
GS FLT4 OS
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OC BUKATY
Matches
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Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 2.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS50011; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS00240; RECEPTOR_TYR KIN III; 1.
Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding; Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                              Finnerty H., Kelleher K., Morris G.E., Bean K., Merberg D.M., Kriz R., Morris J.C., Sookdeo H., Turner K.J., Wood C.R.; Molecular cloning of murine FLT and FLT4."; Oncogene 8:2298.1933).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases.
-(SF-1/PDGF receptor subfamily.
-!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
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VASCULAR ENDOTHELIAL GROWTH FACTOR
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C3-TYPE 7.
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PIR; I58375; I58375.
HSSP; PI1362; 1FGK.
HSSP; PGGS561; Flt4.
GO; GO:0005515; F:protein binding; IPI.
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InterPro; IPR003598; Ig_c2.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001824; RecepttyrkinsIII.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
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                                                                                                                                                                                                                        MEDLINE=93330572; PubMed=8393164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
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1363
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                                                                                                                                   SEQUENCE FROM N.A.
                                               NCBI_TaxID=10090;
                                                                                                                                                                                   STRAIN=C57BL/6J;
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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HSSP; P49962; 1014.
InterPro; IPR008032; SRP9.
InterPro; IPR008018; SRP9/14.
Pfam; PF05486; SRP9; 1.
Signal Procgnition particle; RNA-binding.
103 Aa; 12077 MW; B6EF4A9DA77C13BE CRC64;
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N-LINKED (GLCNAC. . ) (
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16-OCT-2001 (Rel. 40, Last annotation update)
Signal recognition particle 9 kDa protein (SRP9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
46;
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Pred. No. 46;
1; Mismatches
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POTENTIAL
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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Best Local Similarity
Matches 6; Conserv
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ID SR09_MAIZE
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Length 103;

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60.0%; Score 39;

Query Match

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54.5%; Pred. No. 4.2;
           Mismatches
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            6; Conservative
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DSWEEFVERSV 15
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Best Local Similarity
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June 9, 2004, 15:43:00; Search time 40.2162 Seconds (without alignments) 94.147 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
3: sp_fungi:*
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5: sp_invertebrate:*
6: sp_marmmal:*
7: sp_mc:*
8: sp_organelle:*
9: sp_phage:*
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65
1 DDSWVEFIELDI 12
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	O863n9 arctonyx co		_			aonyx					-			_	-	mart on
SUMMAKIES			A	Q863N9	906980	Q863P4	086303	086302	086309	086308	086307	086305	086304	086301	086300	Q863P9	0863P8	Q863P7	0863P6
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			Watch Length DB	101	105	105	106	106	107	107	107	107	107	107	107	107	107	107	107
	ф	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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105 AA.

PRT;

PRELIMINARY;

RESULT 2 QB63Q6 ID Q863Q6

Query Match
100.0%; Score 65; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 12; Conservative 0; Mismatches 0; Indels

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1007 1007 1007 1007 1007 1007 1007 1007	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	T 1 0863N9 0863N9; 0863N9; 0863N9; 01-UUN-2003 (TrEMBLrel. 24, C 01-UUN-2003 (TrEMBLrel. 25, I Growth hormone receptor (Frag GHR. Arctoryx collaris. Arctoryx collaris. Arctoryx collaris; CENARYOLA; Metazoa; Chordata; Mammalia; Eutheria; Carnivora Arctoryx. (1) CENARYOLA; Metazoa; Mammalia; Eutheria; Carnivora Arctoryx. MCDBL TaxID=139309; (1) SEQUENCE FROM N.A. "Type-1 STS Markers Are More Phylogenetic Reconstruction of Syst. Biol. 0.0-0(2003). EMBL; AF498204; AAP19695.1; -G GO, GO:0004872; F:receptor ac Receptor. I 1 NON TER 101 AA; 11428 MW;
	100.0	T 1 99 9063N9 PRELIMINARY C863N9; 01-UUN-2003 (TrEMBLrel. 01-CTC-2003 (TrEMBLrel. 01-CTC-2003 (TrEMBLrel. Growth hormone receptor GHR. Arctonyx collaris. Eukaryota; Metazoa; Cho Mammalia; Eutheria; Car Arctonyx. [1] SEQUENCE FROM N.A. "Type-1 STS Markers Are Phylogenetic Reconstruc "Type-1 STS Markers Are Phylogenetic Reconstruc Syst. Biol. 0:0-02003) EMBL; AF498204; AAP1969 GO; GO:0004872; F:recep GO; GO:0004872; F:recep NON TER 101 SEQÜENCE 101 AA; 114;
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Koepfii K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 bylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF499190; AAP19681.1;
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
                                                                                       Lutra lutra (European river otter).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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106 AA; 12003 MW; EFBODDAEA24C29FF CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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100.0%; Pred. No. 0.00057;
ive 0; Mismatches 0;
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EMBL; AF498191; AAP19682.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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Best Local Similarity 100.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).
EMBL; AF498187; AAP19678.1; -...
GO: GO:0004872; F:receptor activity; IEA.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
                                                                                                          Lontra canadensis (River otter) (Lutra canadensia).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae;
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105 AA; 11879 MW; F6F6445250DB79BF CRC64;
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105 AA; 11852 MW; F07A7052451EB8E7 CRC64;
                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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EMBL; AF498199; AAP19690.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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01-OCT-2003 (TrEMBLrel. 25, Last and
Growth hormone receptor (Fragment).
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NCBI_TaxID=76717;
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498184; AAP19675.1; -.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).",
Syst. Biol. 0:0-0(2003).
EMBL, AF498185; AAP19676.1; -...
GO: GO:0004872; F:receptor activity; IBA.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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107 AA: 12101 MW; 7F3D579D3C26011B CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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100.0%; Pred. No. 0.00057;
tive 0; Mismatches 0;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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                                                                                                                Aonyx capensis (Cape clawless otter)
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:00 (2003).
EMBL; AF498186; AAP19677.1; -.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0.0-0(2003).
EMBL; AF498188; AAP19679.1;
GO: GO:0004872; F: receptor activity; IEA.
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                                                                                                           Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lontra felina (Sea cat) (Lutra felina).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
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107 A2, 12151 MW; 84DD579D3C2EA9FB CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Growth hormone receptor (Fragment).
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                                                                                    Enhydra lutris (Sea otter).
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hes 12; Conservative
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Matches 12; Conservative
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Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Bio., 0:0-0(2003).
EMBL; AR498194; AAP19685.1; -.
GO, GO:0004872; F:receptor activity; IEA.
                                                                                                                                                              Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AR498193; AAR19684.1; -.
GO, GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mustela frenata (Long-tailed weasel).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
           Mustela erminea (Ermine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
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107 AA; 12140 MW; 96DBD146450149FE CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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100.0%; Pred. No. 0.00057;
iive 0; Mismatches 0;
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Best Local Similarity 100.vv
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Matches 12; Conservative
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Q863P8
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Q863P9
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498189; AAP19680.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koepfli K.-P., Wayne R.K., Trype-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae;
                                     Lontra longicaudis (Neotropical otter) (Lutra longicaudis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
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107
107 AA; 12166 MW; 9113E14645IEA8BB CRC64;
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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EMBL; AF498192; AAP19683.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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01-JUN-2003 (TrEMBLrel. 24, Created)
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01-JUN-2003 (TrEMBLrel. 25, Last am
Growth hormone receptor (Fragment).
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Growth hormone receptor (Fragment)
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Matches 12; Conservative
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01-JUN-2003 (TrEMBLrel.
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                                                                                                                        NCBI_TaxID=71113;
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL, AF498195; AAP19686.1; -...
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(2003).

EMBL; AF498196; AAP19687.1; -.
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Mustela vison (American mink).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martes americana (American marten).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
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107 107
107 AA: 12149 MW; 96CCE146450149FE CRC64;
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107 107
107 AA; 12172 MW; 96DBD14658B649FE CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
GHR.
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                                                                                                                               NCBI_TaxID=9667;
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Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model June 9, 2004, 15:36:10 ; Search time 50 Seconds (without alignments) 56.510 Million cell updates/sec Run on:

US-09-660-302D-3 55

1 DSWVEFIELD 10 Sequence:

Perfect score:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* geneseqp2003as:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query	Length	DB	ID	Description
-	55	100.0	12	2	AAY32789	Aav32789 Growth ho
73	55	100.0	130	(1		
e	55	100.0	637	Н	AAP92108	Human c
4	55	100.0	638	П	AAP81326	
2	52	100.0	638	+~1	AAP81327	7 Rabbit
9	55	100.0		Н	AAP92107	7 Rabbit
7	52	100.0	638	7	AAW33394	4 Human o
60	55	100.0		7	AAW33395	
σ	52	100.0	638	7	ADD45061	1 Rat Pro
10	55	100.0	638	7	ADD45067	
11	52	100.0	638	۲	ADD45063	
12	52	100.0	638	7	ADD45065	LO
13	55	100.0	648	4	ABB11437	
14	51	92.7	638	7	AAR06473	~
15	49	89.1	12	(1)	AAY32793	3 Growth
16	49	89.1	12	7	AAY32794	_
17	49	σ	608	~	AAR25246	_
18	43	78.2	705	Ŋ	ABB77350	
19	42	76.4	1399	9	ABU41685	Protein
20	42	76.4	1409	9	ABU39890	0
21	40	72.7	1363	4	AAB37607	Human pr
22	40	72.7	1363	9	ABU04285	
23	39	70.9	14	9	ADA09064	Lantha
24	39	70.9	163	7	AAW20448	
25	39	70.9	255	n	AAB53166	Mac

Aaw20847 H. pylori	Aar40027 Chelator	Aag43966 Zea mays	Aag40846 Zea mays		-	Aag52493 Arabidops	Aag52492 Arabidops		Aar90528 FLT4 rece		Human	Amino			Human	Abu07853 Human vas	Abu04292 Human exp	Human	Human
AAW20847	AAR40027	AAG43966	AAG40846	AAG43965	AAG52494	AAG52493	AAG52492	AAR85937	AAR90528	AAY90365	AAY70746	AAB30542	AAY97785	AAY97575	ABG32043	ABU07853	ABU04292	ABU04307	ABU04298
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39	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
26	27	28	29	30	31	32	33	34	35	36	37	38	3 ð	40	41	42	43	44	45

ALIGNMENTS

Growth hormone receptor; signal transduction; proteolytic cleavage; ubiquitin; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS. Growth hormone receptor polypeptide for inhibition of receptor cleavage. AAY32789 standard; peptide; 12 AA. (first entry) 09-NOV-1999 AAY32789;

Mammalia.

EP943624-A1.

22-SEP-1999.

98EP-00200799. 12-MAR-1998;

98EP-00200799. 12-MAR-1998;

(UYUT-) RIJKSUNIV UTRECHT.

WPI; 1999-510568/43.

Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

Claim 11; Page 27; 36pp; English.

This sequence is from the intracellular domain of the growth hormone receptor. This sequence is an example of a binding site motif AAY32790. This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage results cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding motif, of which this sequence is an example, is located at or around a ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, ursemia, clabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after

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AAP81326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal transduction; proteolytic cleavage; growth hormone receptor; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency.
                                                                                                                    Gaps
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                                                                            Length 12;
                                                                          100.0%; Score 55; DB 2; Length 12
100.0%; Pred. No. 0.011;
live 0; Mismatches 0; Indels
stress and during neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                         Growth hormone receptor polypeptide.
                                                                                                                                                                                                                                                                                                    AAY32792 standard; peptide; 130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 5; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98EP-00200799
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                      Conservative
                                                                                                                                                             1 DSWVEFIELD 10
                                                                                                                                                                                                   2 DSWVEFIELD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-510568/43.
                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130 AA;
                                      Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999
                                                                                  Mac
Local Sim-
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP943624-A1.
                                                                                                                                                                                                                                                                                                                                             AAY32792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia.
                                                                              Query Match
                                                                                                                      Matches
                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                   AAY32792
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An animal can be immunised against its growth hormone receptor by vaccinating against a growth hormone receptor extracellular domain deriv. predetermined to raise polyclonal antisera which affect the receptor as a growth hormone agonist. This method enables continuous growth of target tissues without frequent hormone admin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating growth hormone receptor activity - by immunising animal against growth hormone receptor extracellular domain deriv. to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 1; Length 637; 100.0%; Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spencer SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth hormone receptor; gigantism; acromegaly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martin DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2a-c; 18pp; English.
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1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP81326 standard; protein; 638 AA.
                                                                                                            AAP92108 standard; protein; 637 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human growth hormone receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                  87US-00061942.
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86US-00861236.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammonds RG, Leung DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 DSWVEFIELD 349
                                                                                                                                                                                                                                                      Growth hormone receptor
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                  62
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WPI; 1989-300419/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 637 AA;
                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1986;
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Gaps

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Query Match Best Local S

Matches

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                                                                                        The sequence was deduced from a clone isolated from a rabbit liver cDNA lambda gtll library. The DNA can be inserted into an expression vector for prodn. of the recombinant GRR which is used to treat GH-related disorders such as gigantism and acromegaly. A hydropathy plot revealed an extracellular GH binding domain, a transmembrane domain, and an intracellular signalling domain. Bight potential N-linked glycosylation sites are predicted. See also AAP81126 and AAN81718-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An animal can be immunised against its growth hormone receptor by accinating against a growth hormone receptor extracellular domain deriv. predetermined to raise polyclonal aniegra which affect the receptor as a growth hormone agonist. This method enables continuous growth of target
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                 treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating growth hormone receptor activity - by immunising animal against growth hormone receptor extracellular domain deriv. to rai
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              New pure growth hormone receptor and binding protein - for tr
growth hormone abnormalities, and new encoding DNA sequences.
                                                                                                                                                                                                                                             100.0%; Score 55; DB 1; Length 638; 100.0%; Pred. No. 0.71; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spencer SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissues without Frequent hormone admin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1a-c; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAP92107 standard; protein; 638 AA.
                                                             Disclosure; Page ?; 1pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Growth hormone receptor; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit growth hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-00061942.
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86US-00861236.
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                              DSWVEFIELD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hammonds RG, Leung DW,
                                                                                                                                                                                                                                                                                                           1 DSWVEFIELD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-300419/41.
                                                                                                                                                                                                                                                           Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                    Sequence 638 AA;
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                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                  The sequence was deduced from a clone isolated from an adult liver cDNA lambda gill library. The DNA can be inserted into an expression vector for prodn. of the recombinant GHR which is used to treat GH-related disorders such as gigantism and acromegaly. A hydropathy plot revealed an extracellular GH binding domain, a transmembrane domain, and an intracellular signalling domain. Eight potential N-linked glycosylation sites are predicted. See also AAPB1327 and AANB1718-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                        New pure growth hormone receptor and binding protein - for treating growth hormone abnormalities, and new encoding DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 1; Length 638; 100.0%; Pred. No. 0.71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth hormone receptor; rabbit; gigantism; acromegaly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
/label= signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .18
/label= signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                 Wood WI;
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                                                                                                                                                                                                                                                                                                    Disclosure; Page ?; 1pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit growth hormone receptor.
                                                                                        88WO-US002008
                                                                                                                     87US-00062542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                 Leungh D,
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                                                                                                                                                   (GETH ) GENENTECH INC
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N-PSDB; AAN81717.
                                                                                                                                                                                                               WPI; 1988-368632/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                             N-PSDB; AAN81716
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 638 AA;
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                                                                                                                                                                               Hammonds RG,
                                                                                        10-JUN-1988;
                                                                                                                     12-JUN-1987;
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                              WO8809818-A.
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                                                          15-DEC-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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à g (revised)
(first entry)

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Growth hormone receptor; growth hromone binding protein; somatotropin; rabbit; gigantism; acromegaly; therapy.
                                                                         AAW33395 standard; protein; 638 AA.
                                                                                                                                          Rabbit growth hormone receptor
                         340 DSWVEFIELD 349
        1 DSWVEFIELD 10
                                                                                                                                                                                                                                                                                                                                     25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                       12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                28-JUN-1991;
08-JAN-1993;
                                                                                                              25-MAR-2003
11-MAY-1998
                                                                                                                                                                                                                                                                                                US5688763-A.
                                                                                                                                                                                                                                                                                                                  18-NOV-1997
                                                                                           AAW33395;
                                                                                                                                                                                                                                                                                                                                                                                           (LEUN/) 1 (HAMM/) 1
                                                                                                                                                                                                                                                                                                                                                                                                            (WOOD/) (SPEN/)
                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                     Domain
                                                       RESULT 8
                                                                 AAW33395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This protein sequence comprises human growth hormone receptor. The amino acid sequence was deduced from cDNA clones (see AAT94065) obtained from a human liver cDNA library, and shows 84% identity to the rabbit growth hormone receptor (see AAM93395). Human growth hormone receptor, its deleted, and growth hormone binding proteins comprising amino acids 190-246 or 1-224 of the mature protein, can be used to treat disorders associated with growth hormone over-expression, e.g. gigantism and scromegaly. The binding protein may also be used to increase the stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human and rabbit growth hormone receptor protein - useful to treat disorders associated with overexpression, e.g. gigantism and acromegaly.
                                                                                                                                                    Growth hormone receptor; growth hromone binding protein; somatotropin; human; gigantism; acromegaly; therapy.
                                                                                                                                                                                                                                                          /note= "translated codon is Ser in clone ghr.210 and
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hammonds RG,
                                                                                                                                                                                                                               247. .269
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                     ghr.110, Ile in ghr.501
                                                                                                                                                                                                           1. .18
/label=_Sig_peptide
                                                                                                                                                                                                  iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Leung DW,
                                                                AAW33394 standard; protein; 638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 8a; 60pp; English.
                                                                                                                                 Human growth hormone receptor.
                                                                                                                                                                                                                                                                                                                                                      91US-00723358.
                                                                                                                                                                                                                                                                                                                                              87US-00062542
                                                                                                                                                                                                                                                                                                                            94US-00248832
                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Colosi PC, Spencer SA,
                 340 DSWVEFIELD 349
1 DSWVEFIELD 10
                                                                                                                                                                                                                                                                                                                                                                                  LEUNG D W.
HAMMONDS R G.
WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-008010/01.
N-PSDB; AAT94063.
                                                                                                                                                                                                                                                                                                                                                                                                                        SPENCER S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 638 AA;
                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                            25-MAY-1994;
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                              12-JUN-1987;
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                                                                                                                                                                                                                                                                                                                                                               08-JAN-1993;
                                                                                                                                                                                                                                                                                       US5688763-A.
                                                                                                     25-MAR-2003
11-MAY-1998
                                                                                                                                                                                                                                                                                                        18-NOV-1997
                                                                                   AAW33394;
                                                                                                                                                                                                                                                                                                                                                                                 (LEUN/) 1
(HAMM/) 1
(WOOD/) 1
                                                                                                                                                                                                                                                                                                                                                                                                             (COLO/)
                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                               Domain
                                              RESULT 7
                                                        AAW33394
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This protein sequence comprises rabbit growth hormone receptor. The amino acid sequence was deduced from cDNA clones (see AAT94064) obtained from a rabbit liver cDNA library, and shows 84% identity to the buman growth hormone receptor (see AAW3394). Rabbit and human growth hormone receptors, their derivatives in which the cytoplasmic or transmembrane domains are deleted, and growth hormone binding proteins comprising amino acids 190-246 or 1-324 of the mature proteins, can be used to treat disorders associated with growth hormone over-expression, e.g. gigantism and acromegaly. The binding protein may also be used to increase the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and acromegaly. The binding protein may also be used to increase the stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
                                                                                                                                       /note= "translated codon is Ala in clone ghr.435, Thr in
ghr.440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein - useful to treat . e.g. gigantism and acromegaly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leung DW, Hammonds RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
0.71;
                                                                                                                                                                                                                       247. .269
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human and rabbit growth hormone receptor g
disorders associated with overexpression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55;
Pred. No.
                                                                                   1. .18
/label= Sig_peptide
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 8b; 60pp; English.
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91US-00723358.
93US-00002489.
                                                                                                                                                                                                                                                                                                                                                                                                             94US-00248832
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HAMMONDS R G.
WOOD W I.
COLOSI P C.
Oryctolagus cuniculus.
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Best Local Similarity
                                                                                                                                    Misc-difference 49
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Gaps

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Query Match 100.0%; Score 55; DB 2; Length 638; Best Local Similarity 100.0%; Pred. No. 0.71; Matches 10; Conservative 0; Mismatches 0; Indels

Sequence 638 AA;

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                                                                                                                                                                                                                                                                                                                                       Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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Mismatches
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                                                                                                                                                                                                                                                                                                 Rat Protein P16310, SEQ ID NO 10493.
                                                                                                                                                                              ADD45061 standard; protein; 638 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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  10; Conservative
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                                       1 DSWVEFIELD 10
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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comprising the present an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound or an animal of one or more of the polypeptides given in the setivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating
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                                        Gaps
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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100.0%; Score 55; DB 7; Length 638; 100.0%; Pred. No. 0.71;
                                      Indels
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                                                                                                                                                                                                               ADD45067 standard; protein; 638 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
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GENBANK; P10912.
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              Local Similarity
nes 10; Conserv
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Matches
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a paramaceutical composition, a method for identifying a compound useful in the cativity in an animal of one or more of the polypeptides given in the expression of a method for identifying a compound useful in the cativity in an animal of one or more of the polypeptides given in the cativity in an animal of one or more of the polypeptides given in the cativity in a method for identifying a compound useful in treating
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the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                               100.0%; Score 55; DB 7; Length 638; 100.0%; Pred. No. 0.71; ive 0; Mismatches 0; Indels
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                                                                  ftp.wipo.int/pub/published pct sequences.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                            Sequence 638 AA;
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      the compound that
polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastesis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; lymphoid cell disorder; asthma; arthritis; atherosclerosis; coronary heart disease; arterial ischaemia; hone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiantlammatory; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB11437 standard; peptide; 648 AA.
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27-APR-2000; 2000US-00560875.
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Matches 10; Conservative
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by tentual unexapetute applications. The polypeptides of the invention may differential unexapetute applications. The polypeptides of the invention activities, including cytokine, cell proliferation or cell differentiation activities, stem cell growth actor activity; haematopoiesis regulatory activity; tissue growth activity; conditions care receptor or inhibin-related activities; chemocactic or chemokinetic activities, haemastatio, thrombotic or thrombolytic activities; ancer cell proliferation or metastasis. Chemocancesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myploid or lymphoid cell disorders (e.g., myploid or lymphoid cell disorders (inflammatory conditions (e.g., asthma or arthritis), crancers, haematopoletic disorders (e.g., myploid or lymphoid cell disorders disorders (e.g., myploid or promote wound crancerial ischaemia, bone disorders (e.g., myploid or promote wound crepair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunombulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Common tells in culture to give rise to neuroepithelial cells can promote cell growth. For example, such polypeptides may be used to autoimmune disease or accidental danage. The present sequence represents a novel human conditions, and in drug screening techniques. The present sequence represents a novel human condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent mucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a muclectide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Somatotropin receptor; SR; somatotropin binding protein; SBP; pRAT7-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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/label= divergence
/note= "non-homology region with SBP/pRTA1-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 4; Length 648; 100.0%; Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serum somatotropin receptor protein from clone pRAT7-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264. .289
/label= transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/label=_signal_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR06473 standard; protein; 638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 DSWVEFIELD 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-2003
04-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                            Homology comparison between this putative rat somatotropin receptor and the published sequence indicates 70% identity. See also AAQ05689-91, AAQ06124 and AAQ05700. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal transduction, proteolytic cleavage; growth hormone receptor; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin; growth hormone deficiency.
                                                                                                                                                                                      Somatotropin binding protein and gene - used to regulate and/or modify activity of somatotropin in humans and animals.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                    Length 638;
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                   Score 51; DB 2;
Pred. No. 3.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth hormone receptor derived polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY32793 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5; 36pp; English
                                                                                                                                                                                                                        Disclosure; Fig 6; 43pp; English.
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                                                                                                      (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                                                                                                                                   92.7%;
90.0%;
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                                                         90EP-00102552
                                                                                 89US-00310725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                              Baumbach WR;
                                                                                                                                                                                                                                                                                                                                                                  1 DSWVEFIELD 10
                                                                                                                                                   WPI; 1990-255493/34.
N-PSDB; AAQ05691.
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                                                                                                                                                                                                                                                                                             Sequence 638 AA;
                                                         09-FEB-1990;
                                                                               17-FEB-1989;
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                                  22-AUG-1990
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           EP383205-A.
                                                                                                                             Logan JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY32793;
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qq
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June Run on:

9, 2004, 15:43:40 ; Search time 11.0811 Seconds (without alignments) 86.807 Million cell updates/sec

US-09-660-302D-3 55 1 DSWVEFIELD 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	somatotropin recep					1		14	storage protein 2	vascular endotheli	protein-tyrosine k	hypothetical prote	_	hypothetical prote	Н	_	hypothetical prote	σ	protein-tyrosine k	conserved hypothet	hypothetical prote	- 1	protein C45G9.5 [i	nikkomycin biosynt	probable membrane	homeobox protein A	hypothetical prote	-4	~
SUMMARIES		333	35	A33991	7	\$12136	833608	\$32823	A61619	A34287	JC4954	158375	AG2426	H71924	B64589	866916	T03951	875238	T36175	A48999	B87468	B69951	T50354	C88448	A97993	729	T05850	70	7478	A59095
	DB	7	7	7	(7	7	7	7	7	7	N	7	7	7	7	7	7	7	~	7	~	~	7	~	7	7	~1	7	7	7
	Length	634	638	638	638	638	677	608	702	704	1379	1363	217	321	321	411	103	363	840	1298	208	243	268	316	399	694	718	155	210	259
di	Query	100.0	100.0		100.0			89.1	83.6	74.5			70.9		ö			67.3	67.3		65.5	•	'n.	ď.	٠	ω.	•	ω.	<u>.</u>	63.6
	Score	55	55	55	55	55	52	49	46	41	41	40	39		39	39	38	37	37	37	36	36	36	36	36	36	36	35	35	35
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hypothetical prote	hypothetical prote	hypothetical prote	site-specific DNA-	hypothetical prote	hypothetical prote	probable tRNA aden	phosphoglucomutase	phosphomannomutase	crooked neck-like	Id-associated prot	probable homeodoma	hypothetical prote	3',5'-cyclic-GMP p	3',5'-cyclic-GMP p	3',5'-cyclic-GMP p
G84731	T29966	T48291	S35614	T21823	F82557	T00778	D95174	F98040	T45742	A57591	C84732	G86186	S13032	A36617	A42828
~1	~	~	7	N	~	N	~	N	~	N	~	N	~	α	~
297	387	456	525	537	544	555	572	572	599	621	721	749	800	853	854
63.6	63.6	63.6	63.6	63.6	9.69	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6	63.6
35 63.6	35 63.6						35 63.6								

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Figure T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.
Mol. Cell. Endocrinol. 73, 135-145, 1990
A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expra A;Reference number: S33339; MUID:91099608; PMID:1980117
A;Reference number: S33339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-634 <ADD>
A;Cross-references: EMBL:M82912; NID:g165888; PIDN:AAA73171.1; PID:g165889
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
                                           N;Alternate names: growth hormone receptor
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 02-Aug-2002
C;Accession: S33339
somatotropin receptor - sheep
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0 Gaps .. 100.0%; Score 55; DB 2; Length 634; ilarity 100.0%; Pred. No. 0.05; Conservative 0; Mismatches 0; Indels 0; Indels Query Match Best Local Similarity Matches 10; Conserv

DSWVEFIELD 345 1 DSWVEFIELD 10 336 Ωp ò

RESULT 2

somatotropin receptor precursor - rat
NyAlternate names: growth hormone receptor
C;Species: Rattus norvegicus (Norway rat)
C;Decies: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 02-Aug-2002
C;Accession: A32985; A33505
R;Baumbach, W.R.; Horner, D.L.; Logan, J.S.
Genes
A;Title: The growth hormone-binding protein in rat serum is an alternatively spliced for A;Reference number: A32985; MUID:90006741; PMID:2792761

A; Accession: A32985

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-638 <BADA A;Cross-references: GB:X16726

R.Mathews, L.S.; Enberg, B.; Norstedt, G. J. Biol. Chem. 264, 9905-9910, 1989 Affitle: Regulation of rat growth hormone receptor gene expression. A;Reference number: A33505; MUID:89255563; PMID:2722883

A;Accession: A33505 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-638 https://doi.org/10.1007/pdf A;Residues: 1-638 https://doi.org/10.1007/pdf A;Cross-references: GB:J04811; NID:g204308; PIDN:AAA41219.1; PID:g204309

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RESULT 6
S33608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A33991; S04530 K:Gacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; Korconski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; Koroc, Natl. Acad. Sci. US.A. 86, 8083-8087, 1989
A;Title: Characterization of the human growth hormone receptor gene and demonstration of A;Reference number: A33991; MUID:90046742; PMID:2813379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; GB R,Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.; Mature 3330, 537-543, 198.
A,Title: Growth hormone receptor and serum binding protein: purification, cloning and ex A,Reference number: 804530; MUID:88065896; PMID:2825030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sometoropin receptor precursor, hepatic - rabbit

NyAlternate names: growth hormone receptor

NyContains: sometotropin-binding protein, serum

NyContains: sometotropin-binding protein, serum

NyContains: sometotropin-binding protein, serum

NyContains: sometor, suniculus (domestic rabbit)

CyBecies: Oryctolagus cuniculus (domestic rabbit)

CyBecies: Oryctolagus cuniculus

CyBecies: Oryctolagus

CyBecies: Oryctolagus

CyBecies: Oryctolagus

NyTitle: Growth hormone receptor and serum binding protein: purification, cloning and ex

AyReference number: S04530; MUID:88065896; PMID:2825030
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C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: liver; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-60aduct: somatotropin recentor #nt-1-1
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-638 cLEU>
A;Residues: 1-638 cLEU>
A;Cross-references: GB:AF015252; NID:g2342651; PIDN:AAB67613.1; PID:g2342652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 02-Aug-2002
                                                                                                                                                           Gaps
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A,Molecule type: mRNA
A,Residues: 1-543. "1.545-638 <LEUS
A,Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738
C,Genetics:
A,Gene: GDB:GRR
A,Cross-references: GDB:119984; OMIM:600946
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                                                                                               Length 638;
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;1-18/Domain: signal sequence #status predicted <SIG>
;19-638/Product: somatotropin receptor #status predicted <MAT>
;265-288/Domain: transmembrane #status predicted <TVM>
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                                                                                            Score 55; DB 2;
Pred. No. 0.051;
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100.0%; Pred. No. 0.051;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N'Alternate names: growth hormone receptor N'Contains: somatotropin-binding protein, serum
                                                                                                                                                           0; Mismatches
                                                                                            100.0%;
100.0%;
                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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A; Residues: 1-638 <GOD>
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A;Status: preliminary
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Cjoate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Aug-2002
Cjoate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Aug-2002
Cjacession: 833609, 333607
R;Smith, W.C.; Kuniyoshi, J.; Talamantes, F.
A;Emith, W.C.; Kuniyoshi, J.; Talamantes, F.
A;Title: Mouse serum growth hormone (GH) binding protein has GH receptor extracellular A;Reference number: 833607; MuID:89295449; PMID:2739661
A;Accession: 833608
A;Accession: 833608
A;Molecule type: mRNA
A;Residues: 1-677 < SMI>A;Cross-references: EMBL:M33324; NID:g193508; PIDN:AAA37690.1; PID:g3309253
A;Note: part of this sequence, including the amino end of the mature protein, was confinencer, S.A.; Hammonds, R.G.; Henzel, W.J.; Rodriguez, H.; Waters, M.J.; Wood, W.I. J. Biol. Chem. 263, 7862-7867, 1988

A;Title: Rabbit liver growth hormone receptor and serum binding protein. Purification, A;Reference number: 92972; MUID:8227992; PMID:3372509

A;Accession: B28176

A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: A28176
A,Molecule type: protein
A,Rolecule type: protein
C,Superfamily: interleukin-2 receptor beta chain, fibronectin type III repeat homology
C,Keywords: glycoprotein; liver; transmembrane protein
F;1-18/Domain: signal sequence #status predicted ASIG-F;1-8/Ponduct: somatotropin receptor #status experimental AMI>F;265-288/Domain: transmembrane #status predicted ATMN>F;265-288/Domain: carbohydrate (ASI) (covalent) #status experimental
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C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein
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C;Species: Sus scrofa domestica (domestic pig)
C;Dacte: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S12136
R;Cioffi, J.A.; Wang, X.; Kopchick, J.J.
Nucleic Acids Res. 18, 6451, 1990
A;Title: Porcine growth hormone receptor cDNA sequence.
A;Title: Porcine growth hormone receptor cDNA sequence.
A;Reference number: S12136; MUID:91057155; PMID:2243805
A;Accession: S12136
A;Accession: S12136
A;Accession: S12136
A;Accession: G1236
A;Accession: G1236
A;Accession: G1236
A;Accession: G1236
A;Residues: 1-638 cCIO>
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0; Mismatches
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10; Conservative 0
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Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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storage protein 2 - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 04-Sep-1998
C;Accession: A34287
R;Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.
A;Fujii, T. Sakurai, B.; 1989 A;Fithe: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mg A;Reference number: A34287; MUID:89291839; PMID:2544581
                                                                                              A.Accession: A61619
A.Molecule type: DNA
A.Molecule the authors' translation, residue 306-Leu is omitted, residue 317-Asn is dup
C.Genetics:
A.Note: single copy gene
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A; Kesidues: 1-1379 < EIC.

A; Cross-references: EMBL: X83287; NID:g619865; PIDN:CAA58267.1; PID:e283815; PID:g1707416

C; Comment: This protein is an endothelial-specific receptor and binds vascular endothel:

C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C; Keywords: ATP: embryo; growth factor receptor; transmembrane protein

F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 789-810/Domain: transmembrane #status predicted <TWM>
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A,Reference number: JC4953; MUID:97017121; PMID:8863722
A,Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellone. A,Reference number: A61619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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C, Keywoods: glycoprotein; hemolymph; storage protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;21,481/Pinding site: carbohydrate (Asn) (covalent) #status predicted
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R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M
Gene 174, 3-8, 1996
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Pred. No. 19;
3; Mismatches
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Matches 7; Conservative
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544 DNWMKFFELD 553
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Matches 6; Conserv
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A;Status: preliminary
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N;Alternate names: growth hormone receptor
N;Contains: somatotropin receptor, short form
C;Species: allus gallus (chicken)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 02-Aug-2002
C;Accession: S32823; A49812
C;Accession: S32823; A49812
Endocrinology 128, 1391
A;Furnaide, J; iiou, S.S.; Cogburn, L.A.
Endocrinology 128, 13183-3192, 1391
A;Fitle: Molecular cloning of the chicken growth hormone receptor complementary deoxyrib
A;Reference number: S32823; MUID:91243665; PMID:2036984
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A;Residues: 1-109 «HUA»
A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138
A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138
A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138
A;Cross-references: GB:S68576; NID:g49676; GB:G57676 GB:G57
         A;Experimental source: liver
A;Accession: $33607
A;Accession: $33607
A;Accession: $33607
A;Accession: $33607
A;Corough a;Accession: $23607
A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252
A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252
A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252
C;Superfamally: interleukin-2 receptor; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-677/Product: somarcotropin-binding protein, high molecular weight #status predicted F;274-297/Domain: transmembrane #status predicted <TWM>F;274-297/Domain: cransmembrane #status predicted <TWM>F;40,169/Bainding site: carbohydrate (Asn) (covalent) #status predicted
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A;Status: preliminary
A;Molecule type: mRNA
A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811
A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811
A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811
Mol. Endocrinol. 7, 1391-1398, 1993
A;Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf
A;Reference number: A49812; MUID:94158898; PMID:8114754
A;Accession: A49812
A;Accession: A9812
A;Molecule type: mRNA
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C;Species: Galleria mellonella (greater wax moth)
C;Date: 21-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999
C;Accession: A61619
R;Memmel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.
Insect Biochem. Mol. Biol. 22, 333-342, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 2; Length 677; 100.0%; Pred. No. 0.054; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%; Score 49; DB 2; Length 608; 90.0%; Pred. No. 0.58; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arylphorin precursor - greater wax moth
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
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à g us-09-660-302d-3.rpr

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hypothetical protein jhp0501 - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
G;Decies: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C;Accession: H71924
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001483; GB:AE001439; NID:g4155034; PIDN:AAD06079.1; PID:g41550
A;Experimental source: strain J99
Genetical source: strain J99
A;Genetipo501
C;Superfamily: Helicobacter pylori hypothetical protein jhp0501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyperacian process relicobacter pylori (Strain 2003);
Cyperacian process relicobacter pylori
Cybaces (Species: Helicobacter pylori
Cybacesion: B64589
Cyfacession: B64589
Cyfacession: B64589
Cyfacession: B64589
Cyfacession: B64589
Cyfacesion: B7: White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Consoling Signature Samplete genome sequence of the gastric pathogen Helicobacter pylori.
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Mesidues: 1-321 < TOM>
A; Mesidues: 1-321 < TOM>
A; Cross-references: GB:AE000569; GB:AE000511; NID:92313663; PIDN:AAD07620.1; PID:923136
C; Superfamily: Helicobacter pylori hypothetical protein jhp0501
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N;Alternate names: hypothetical protein 02762
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul.1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S66916
R;Landt, O.; Hiesel, R.; Unseld, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein HP0554 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.9%; Score 39; DB 2; Length 321; 70.0%; Pred. No. 18; Live 1; Mismatches 2; Indels
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                           182 WVELIELD 189
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-321 < ARN>
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G.Species: Nostoc sp. PCC 7120
A.Note: Nostoc sp. strain PCC 7120
A.Note: Nostoc sp. strain PCC 7120
G.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
G.Accession: Ad448
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tasuda, B. 705-213, 2001
A.Nilano, G. S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tasuda, S.; Watenenic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A.Accession: AG426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1033-1072 <GAL>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase F;843-1176/Domain: protein kinase homology <KIN>F;851-859/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                           protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Feb-2000 C;Accession: IS8375; B42010 R;Pinnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, Oncogene 8, 2293-2298, 1993 A;Fite: Molecular cloning of murine FLT and FLT4. A;Reference number: IS8375; MUID:9330572; PMID:8393164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1363 <RES>
A;Ressidues: 1-1363 <RES>
A;Cross-references: GBiLO7296; NID:g293780; PIDN:AAA40077.1; PID:g293781
A;Cross-references: GBiLO7296; NID:g293780; PIDN:AAA40077.1; PID:g293781
B;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D. Genomics 13, 475-478, 1992
A;Title: Giromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene. A;Reference number: A42010; MUID:92307693; PMID:1319394
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A;Cross-references: GB:BA00019; PIDN:BAB76666.1; PID:g17134105; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                               Gaps
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             Length 1379
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Pred. No. 12;
0; Mismatches 1; Indels
                                                                        0; Indels
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A;Molecule type: mRNA
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      Score 41; DB 2
Pred. No. 38;
2; Mismatches
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Dest Local Similarity 87.5%;
Matches 7; Conservative 0
          74.5%;
75.0%;
                                                                           6; Conservative
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                                                                                                                                                                                                    DIWVEFVE 526
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Query Match
Best Local Similarity
Matches 6; Conserv
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submitted to the Protein Sequence Database, July 1996
A,Recession: $66907
A,Accession: $66916
A,Fesidues: 1411 <LAN>
A,Fors. **references: EMBL:Z74949; NID:g1420165; PID:e251966; PID:g1420167; GSPDB:GN00015;
A,Genetics:
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Search completed: June 9, 2004, 15:52:17 Job time: 12.0811 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 9, 2004, 15:36:55; Search time 7.2973 Seconds (Without alignments) 71.355 Million cell updates/sec Run on:

US-09-660-302D-3 55 1 DSWVEFIELD 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	P79108 bos taurus	575 ovis arie	2 homor	magag		P19941 orvetolagis		_		Q90375 columba liv					shew			caenorhab		saccharomy	_	_		Q99543 homo sapien	_	Q9bzj0 homo sapien	bos t	homo	canig	_	793 mils	50 0000	58145 metha
SUMMARIES	;	ID	GHR BOVIN	GHR SHEEP	GHR HUMAN	GHR MACMU	GHR PIG	GHR RABIT	GHR RAT	GHR_MOUSE	GHR_CHICK	GHR_COLLI	RPOC_PSEPU	SSP2_BOMMO	VGR3_MOUSE	SR09 MAIZE	MURB_SHEON	VGR3 HUMAN	YOEF BACSU	YQI5_CAEEL	Y4FP_RHISN	FRES_YEAST	ZRF1_MOUSE	MTA1_ARTLU	UGTS_CAEEL	ZRF1_HUMAN	CRN1_MOUSE	CRN1_HUMAN	CNRB_BOVIN	CNRB HUMAN	CNRB CANFA	CNRB_MOUSE	PGBM_MOUSE	PGBM_HUMAN	RUB1_METJA
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P26755 saccharomyc	002373 drosophila	O10302 O19yla pseu Q00868 qibberella	P38114 saccharomyc	P24063 mus musculu	Q9wzs9 thermotoga	P82978 lepidosiren	P48345 desulfovibr	P22076 desulforibr	P20418 desulfovibr
RFA3 YEAST HST3 YEAST	UGDH DROME	ESYN GIBPU	YBOO_YEAST	ITAL MOUSE	SYFB_THEMA	S100 LEPPA	DESR DESVM	DESR_DESDE	DESR_DESVH
ПП			7	Н	Н	-	Н	Н	Н
122	476	983	1094	1163	788	75	123	125	125
61.8	61.8	61.8	61.8	61.8	6.09	0.09	0.09	0.09	0.09
3 3 4 4	3. 4. 4.	34	34	34	33.5	33	33	33	33
3.4 3.5	36	38	9.6	0.4	41	42	43	44	45

ALIGNMENTS

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VARIANTS LARON DWARFISM
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111
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196
634 AA;
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BONDS
                                                                                                                                                           HUMAN
                                                                                                                                                                                                                protein).
          CARBOHYD
CARBOHYD
CARBOHYD
                             CARBOHYD
                                     SEQUENCE
                                                                                                                                                           GHR HUM
P10912;
                                                                                                                                                   GHR_HUMAN
                                                                                                                                         RESULT 3
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  FT FT SO
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                  MEDLINE-21099608; PubMed-1980117; Adams T.E., Baker L., Fiddes R.J., Brandon M.R.; "The sheep growth hormone receptor: molecular cloning and ontogeny of
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 35, Last amnotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                Length 634;
                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
           N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PO
91955A28296CBD2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROWTH HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M82912; AAA73171.1; -.
PIR; S3339; S3339.
HSSP; P10912; 1AXI.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
PR00041; FN III.
SMART; SM00060; FN 3; 1.
PROSITE; PS01352; HEMATOPO REC_LF1; 1.
PROSITE; PS01352; HEMATOPO REC_LF1; 1.
SIGNAL.
SIGNAL.
                                                 100.0%; Score 55; DB 1; 100.0%; Pred. No. 0.014;
                                                                    Mismatches
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                                 70979 MW;
                                                          Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                      STANDARD;
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260
284
634
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136
46
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                                                                                       1 DSWVEFIELD 10
    152 1
157 1
196 1
634 AA;
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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19
261
285
141
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Q28575;
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TRANSMEM
DOMAIN
DOMAIN
DISULFID
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CARBOHYD
SEQUENCE
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                                                   Query Match
     CARBOHYD
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Fuh G., Mulkerrin M.G., Bass S., McFarland N., Brochier M., Bourrel J.H., Light D.R., Wells J.A.;
"The human growth hormone receptor. Secretion from Escherichia coli and disulfide bonding partern of the extracellular binding domain.";
J. Biol. Chem. 265:3111-3115(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R., Kerter R., Rotwein P.S., Parks J.S., Laron Z., Wood W.I.; "Characterization of the human growth hormone receptor gene and demonstration of a partial gene deletion in two patients with Larontype dwarfism.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-001-1989 (Rel. 11, Created)
01-001-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93278381; PubMed-8504296;
Amselem S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,
Valleix S., Goossens M.;
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                                                                                                                                                                                                  Length 634;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                            FFD28B9C23EC1496 CRC64;
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                                                                                                                                                                                                      100.0%; Score 55; DB 1; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         638 AA
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT LEU-544.
MEDLINE=90046742; PubMed=2813379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
MEDLINE=88065896; PubMed=2825300;
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MEDLINE=94185645; PubMed=8137822;
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                                                                                                                                            70844 MW;
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Best Local Similarity 100.
Matches 10; Conservative
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M28461; AAA52555.1; JOINED. M28462; AAA52555.1; JOINED. M28463; AAA52555.1; JOINED. M28464; AAA52555.1; JOINED. M28465; AAA52555.1; JOINED.

EMBL; EMBL; PIR; PDB; PDB; PDB; PDB; PDB; PDB;

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VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242. MEDLINE=96013502; PubMed=7565946; Goddard A.D., Covello R., Luoh S.-M., Clackson I., Attie K.M., Gesundheit N., Rundla A.C., Wells J.A., Carlsson I.M.S.; "Mutations of the growth hormone receptor in children with idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of single-nucleotide polymorphisms in coding regions of human genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARTANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579.
MEDLINE=99318093; PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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DISEASE: Defects in GHR are a cause of Laron dwarfism
[MIN:262509]; also known as piruthary dwarfism II (Laron-type
pitulitary dwarfism or Laron syndrome (LS)).
DISEASE: Defects in GHR are a cause of idiopathic short stature
[MIN:600946].
SIMILARITY: Belongs to the type I cytokine family of receptors.
Subfamily 1.
SIMILARITY: Contains 1 fibronectin type III domain.
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"Crystal structure of an antagonist mutant of human growth hormone, gallon, in complex with its receptor at 2.9-A resolution.";
J. Biol. Chem. 271:32197-32203(1996).
Dusquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R.,
Savage M.O., Preece M.A., Craescu C.T., Blouquit Y., Goossens M.,
                                                                                                                "A single amino acid substitution in the exoplasmic domain of the human growth hormone (GH) receptor confers familial GH resistance (Laron syndrome) with positive GH-binding activity by abolishing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de Vos A.M., Ultsch M., Kossiakóff A.A.; "Human growth hormone and extracellular domain of its receptor: crystal structure of the complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.
MEDLINE=97113023; PubMed=8943276;
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MEDLINE=92196577; PubMed=1549776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                short stature.";
New Engl. J. Med. 333:1093-1098(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crystal structure of the complex."
Science 255:306-312(1992).
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                                                                                                                                                                                                                                                     receptor homodimerization.";
                                                                                                                                                                                                                                                                                            EMBO J. 13:1386-1395(1994)
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GO; GO:0004903; F:growth hormone receptor activity; TAS. GO; GO:0007150; P:growth pattern; TAS. GO; GO:0001501; P:skeletal development; TAS. InterPro; IPR002996; CRIA.

Genew; HGNC:4263; GHR.
MIM; 600946; -.
MIM; 262500; -.
GO:00050887; C:integral to plasma membrane; TAS.
GO; GO:0004903; F:growth hormone receptor activity;
GO; GO:0007150; P:growth pattern; TAS.

1HWH; 19-NOV-97. 1AXI; 28-JAN-98. 1A22; 29-APR-98. 1KF9; 20-NOV-02.

A33991, A33991. 3HHR; 30-APR-94. 1HWG; 19-NOV-97.

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/FTIG=VAR 002710.
V -> A (in Laron dwarfism).
V -> A (in Laron dwarfism).
V -> D (in Laron dwarfism).
/FTIG=VAR 002712.
D -> H (in Laron dwarfism);
D -> H (in Laron dwarfism);
FTIG=VAR 002713.
/FTIG=VAR 002713.
R -> C (in Laron dwarfism and idiopathic
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
E -> K (in idiopathic short stature)
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Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure; Dwarfism; Polymorphism; Disease mutation.
SIGNAL
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/FIGEVAR 002714
R -> H (in dbSNP:6181).
/FIId=VAR 013937
R -> G (in Laron dwarfism).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH HORMONE RECEPTOR
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R -> H (in_dbSNP:6177).
/FTId=VAR_013938.
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(in_dbSNP:6180)
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/FTId=VAR 013941
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InterPro; IPR003528; Hemtopoptn_L_F1
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SMART; SM00060; FN3; 1
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EMBL; X06562; CAA29808.1; -.
EMBL; M28466; AAA52555.1; -.
BEBL; M28458; AAA52555.1; JOINED.
EMBL; M28459; AAA52555.1; JOINED.
EMBL; M28460; AAA52555.1; JOINED.

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CARBOHYD
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           Gaps
                                                                                                                                                                                                                                                                                 Martini J.F., Pezet A., Guezennec C.Y., Edery M., Postel-Vinay M.C.,
                                                                                                                                                                                                                                                                                          Kelly P.A.;

"Monkey growth hormone (GH) receptor gene expression. Evidence for monkey growth hormone (GH) receptor gene expression. Evidence for J. Biol. Chem. 272:18951-18958(1997).

-!- FUNCTION: This is a receptor for pituitary gland growth hormone.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.

-!- SIMILARITY: Contains I fibronectin type III domain.
                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
           6
                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 1; Length 638; 100.0%; Pred. No. 0.014;
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           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
 Pred. No. 0.014;
; Mismatches 0;
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Glycoprotein; Signal.
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InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_LF1.
SMART; SM00060; FN3; IPR005178; PS01352; HEMATOPO REC LF1;
Receptor; Transmembrane; Glycoprotein.
                                                                                                          PRT;
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MEDLINE=97373601; Pubmed=9228076;
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                                1 DSWVEFIELD 10
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638 AA;
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Best Local Similarity
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                  STRAIN=Landrace-Yorkshire; TISSUE=Liver;
STRAIN=Landrace-Yorkshire; TISSUE=Liver;
MEDLINE=91057155; PubMed=2243805;
Cloffi J.A., Wang X., Kopchick J.J.;
Porcine growth hormone receptor cDNA sequence.";
Nucleic Acids Res. 18:6451-6451(1990).
-!- FUNCTION: This is a receptor for pituitary gland growth hormone.
-!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
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FIBRONBCTHY TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
                                                                                                                                                                                                                                Bukaryota; MetZzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                         01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subfamily 1.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
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638 AA
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HSSP; P10912; 1A22.
INCEPPO; IPR00296; CRIA.
INCEPPO; IPR003961; FN III.
INCEPPO; IPR003528; Hemcopoptn_L_F1.
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nes 10; Conserv
                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                           01-FEB-1991
15-MAR-2004
                                                                                                                                                             protein).
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RESULT

340 DSWVEFIELD 349

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638 AA

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DOMAIN
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                                                                                                                                                                                          cloning and expression.";
Nature 330:537-543(1987).
-!- FUNCTION: This a receptor for pituitary gland growth hormone.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                           Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C., Henzel W.J., Barnard R., Waters M.J., Wood W.I., "Growth hormone receptor and serum binding protein: purification,
                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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(POTENTIAL).
(POTENTIAL).
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                                   01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 638;
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N-LINKED (GLCNAC. . .) (.
N-LINKED (GLCNAC. . .)
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HSSP; P10912; IA22.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_F1.
Pfam; PF00041; fn3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
Receptor; Transembrane; Glycoprotein; Signal.
SIGNAL
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                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88065896; PubMed=2825030;
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        PRT;
             P19941;
01-FBB-1991 (Rel. 17, Created)
01-FBB-1991 (Rel. 17, Last seq
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                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baumbach W.R., Horner D.L., Logan J.S.;
"The growth hormone-binding protein in rat serum is an alternatively spliced form of the rat growth hormone receptor.";
Genes Dev. 3:1199-1205(1989).
-!-FUNCTION: This is a receptor for pituitary gland growth hormone.
-!-SUBUNIT: Homodimer.
-!-SUBCELLULAR LOCATION: Type I membrane protein.
-!-SUBCELLULAR LOCATION: Type I general protein.
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(COTENTIAL)
(COTENTIAL)
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
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Mathews L.S., Enberg B., Norstedt G.;
"Regulation of rat growth hormone receptor gene expression.";
"D. Biol. Chem. 264:9905-9910(1989).
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EXTRACELLULAR (POTENTIAL)
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FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINED (GLCNAC. ..) (POTENTINE (GLCNAC. ..) (POTENTINE (GLCNAC. ..) (POTENTINE (GLCNAC. ..) (POTENTINE (GLCNAC. ..) (POTENTINE
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SMART; SM00060; FN3; 1.
ROCSITE; PS01352; HEMATOPO REC_L F1; 1.
RECEPCOF; Transmembrane; Glycoprotein; Signal.
SIGNAL
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HSSP; P10912; 1A22.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90006741; PubMed=2792761;
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FUNCTION: Isoform 1 is a receptor for pituitary gland growth hormone. Isoform 2 is a serum growth hormone binding protein that may play an important role in regulating the effective serum concentration of gh.
SUBUNIT: Isoform 1 is a homodimer.
SUBCELIULAR LOCATION: Type 1 membrane protein (isoform 1).
Secreted (isoform 2).
                                                                                                                                                                                                                                                                                                                                  Moffat J.G., Edens A., Talamantes F., "Structure and expression of the mouse growth hormone receptor/growth
                                 GHR MOUSE STANDARD; PRT; 650 AA.
P16882; P16590; Q9R264;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (GH binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou Y., He L., Kopchick J.J.;
"An exon encoding the mouse growth hormone binding protein (mGHBP)
carboxy terminus is located between exon 7 and 8 of the mouse growth
hormone receptor gene.",
Receptor 4:223-227(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=Swiss Webster, and DBA/2J;
MEDLINE=95080157; PubMed=7988474;
MEDLINE=95080157; PubMed=79884774;
Rédens A., Southard J.N., Tanantes F.;
"Mouse growth hormone receptor/binding protein and growth hormone receptor transcripts are produced from a single gene by alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=HMW GHR;
Isoid=P16882-1; Sequence=Displayed;
Name=2; Synonyms=LMW GHR,
Name=2; Synonyms=LMW GHR,
Squence=VSP 001716, VSP 001717;
SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                               Smith W.C., Kuniyoshi J., Talamantes F.; "Mouse serum growth hormone (GH) binding protein has GH receptor extracellular and substituted transmembrane domains."; Mol. Endocrinol. 3:984-990(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE=88288223; PubMed=3398846;
Smith W.C., Colosi P., Talamantes F.;
"Isolation of two molecular weight variants of the mouse growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou Y., He L., Kopchick J.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE=89295449; Pubmed=2739661;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                              hormone binding protein gene."; J. Mol. Endocrinol. 23:33-44 (1999).
                                                                                                                                                                                                                                                                                                           STRAIN=Swiss Webster, and DBA/2J;
MEDLINE=99367316; PubMed=10425445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrinology 135:2802-2805(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95201642; PubMed=7894338;
                                                                                                               (GHBP) (Serum binding protein)
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                                                                                                                                         Mus musculus (Mouse)
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Mol. Endocrinol. 2:1
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                                                                                                                                                                            NCBI_TaxID=10090;
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EIDNHLYHQLQRIRH (in isoform 2).
/FTId=VSP 001716.
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N-LINKED (GLCNAC. .) (POTENTIAL).
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G - A (IN REF. 3 AND 4).

E - G (IN REF. 2).

E - A (IN REF. 2).

R - A (IN REF. 2).

W, 95653380CAF0B931 CRC64;
Subfamily 1. SIMILARITY: Contains 1 fibronectin type III domain.
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PROSITE; PS01352; HEMATOPO REC L F1; 1.
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InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_F1.
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AF120481, AAD32555.1;
AF120483, AAD32555.1; JOINED.
AF120483, AAD32555.1; JOINED.
AF120484, AAD32555.1; JOINED.
AF120486, AAD32555.1; JOINED.
AF120486, AAD32555.1; JOINED.
                                                                                                                                                                                                    AF120485; AAD32556.1; JOINED
AF120486; AAD32556.1; JOINED
AF120487; AAD32556.1; JOINED
AF120488; AAD32556.1; JOINED
                                                                                                                                                                       EMBL; M33324; AAA37690.1; ALT SEQ.
EMBL; M31680; AAA37689.1; ALT_SEQ.
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RESULT 9

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GHR_COLLI
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                                                                                     Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                     sex-linked dwarf chickens.";
Endocrinology 128:3183-3192(1991).
-!- FUNCTION: This is a receptor for pituitary gland growth hormone.
                                                                                                                                                                                                                                                    -!- SUBUNTT: Homodimer.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: Broad specificity.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N.LINKED (GLCNAC. . .) (POTENTIAL).
                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                      Burnside J., Liou S.S., Cogburn L.A.; "Molecular cloning of the chicken growth hormone receptor complementary deoxyribonucleic acid: mutation of the gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 1; Length 608;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                   Subfamily 1.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D71AD7B6C62528DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GROWTH HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, PIOSI2, JAXI.

HSSP, PIOSI2, JAXI.

InterPro; IPR00895; CRIA.

InterPro; IPR008951; FN III-like.

InterPro; IPR003529; Hemtopoptn_L.Fl.

Pfan; PF00041; fn3; 1.

SMART; SM00060; FN3; 1.

Receptor; Transmembrane; Glycoproftein; Signal.

SIGNAL.
  608 AA.
  PRT;
                                                                                                                                                                            MEDLINE=91243665; PubMed=2036984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M74057; AAA48781.1; -. PIR; S32823; S32823.
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90.0%;
  STANDARD;
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608
223
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83
111
86
127
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Best Local Similarity
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
262
1117
34
GHR CHICK
Q02092;
                                                                  protein).
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                                                                                                                                                                                                                                                                  TISSUE-Liver;
Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is a receptor for pituitary gland growth hormone.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                  Columba livia (Domestic pigeon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Columbiformes; Columbidee; Columba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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FIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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  611 AA
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0; Mismatches
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InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_F1.
Pfam: PF00041; fn3; 1.
SWART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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nes 9; Conservative
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174
611 AA;
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0; Mismatches

9; Conservative

Matches

313 DLWVEFIELD 322

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ID SSP2_B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89117617; PubMed=3219133;
Borodin A.M., Danilkovich A.V., Chernov I.P., Azhykina T.L.,
Rostapshov V.M., Monastyrskaya G.S.;
"Genes coding for RNA polymerase in bacteria. III. The use of
modified Sanger's method for sequencing the C-terminal region of rpoB
gene, N-terminal region of rpoC gene and intercistron region of RNA
polymerase in Pseudomonas putida",
Bioorg. Khim. 14:117-1182(1988).
-: FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A. Borodin A.M., Allikmets R.L., Rostapshov V.M., Danilkovich A.V., Borodin A.M., Allikmets R.L., Rostapshov V.M., Chernov I.P., Azhikina T.L., Monastyrskaya G.S., Sverdlov E.D.; Mucleotide sequence of the rpoc gene coding for the beta'-subunit of RNA polymerase in Pseudomonas putida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {RNA}(N).
-!- SUBDAIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
                                                        01-NOV-1990 (Rel. 16, Created)
01-REB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription.
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(IN REF.
                       1409 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000722; RNA_pol_A.
Interpro; IPR007080; RNA_pol_Rpbl_1.
Interpro; IPR007083; RNA_pol_Rpbl_3.
Interpro; IPR007083; RNA_pol_Rpbl_4.
Interpro; IPR007081; RNA_pol_Rpbl_5.
Interpro; IPR007081; RNA_pol_Rpbl_5.
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Pfam; PF00623; RNA POL Rpbl 2; 1.
Pfam; PF04983; RNA POL Rpbl 3; 1.
Pfam; PF049098; RNA POL Rpbl 3; 1.
Pfam; PF04999; RNA POL Rpbl 4; 1.
SMART; SM00663; RPOLA N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X16538; CAA34538.1; -. EMBL; M38319; AAA25987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE OF 1-497 FROM N.A.
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203
328
335
348
482
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HSSP; Q9KWU6; IHQM.
                                                                                                                                                                                         Pseudomonas putida.
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17
203
203
3328
482
                                                                                                                                                                                                                                                     NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substrates.
                     RPOC PSEPU
P19176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Bombycoidea, Bombycidae, Bombyx.
WCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=8221839; PubMed=2544581;

MEDLINE=8221839; PubMed=2544581;

Eujii T., Sakurai H., Izumi S., Tomino S.;

Fujii T., Sakurai H., Izumi S., Tomino S.;

Structure of the gene for the arylphorin-type storage protein SP 2

of Bombyx mori.";

J. Biol. Chem. 264:11020-11025(1989).

I. FUNCTION: Larval storage protein (LSP) which may serve as a store of amino acids for synthesis of adult proteins.

I. SUBCELLULAR LOCATION: Extracellular.

I. TISSUE SPECIFICITY: Fat body.
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEX-SPECIFIC STORAGE-PROTEIN 2.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                           Score 42; DB 1; Length 1409;
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 704;
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84 T -> I (IN REF. 2).
154544 MW; C5662109D3BE3D81 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 37, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                           2; Mismatches
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BIR, A34287, HSSP, P04253; LOXY.
HSSP, P04253; LOXY.
INTERPRO; IPR008922; Di-copper_centre.
InterPro; IPR00892; Hemcoyanin_C.
InterPro; IPR005203; hemcoyanin_C.
InterPro; IPR005204; hemcoyanin_N.
InterPro; IPR00710; Ig-like.
Pfam; PF00372; hemcoyanin; L.
Pfam; PF03722; hemcoyanin, C; L.
Pfam; PF03723; hemcoyanin_C; L.
Pfam; PF03723; hemcoyanin_C; L.
Pfam; PF03722; hemcoyanin_C; L.
Pfam; PF03722; hemcoyanin_C; L.
Pfam; PF03723; hemcoyanin_C; L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sex-specific storage-protein 2 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41;
Pred. No.
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EMBL; M24371; AAA27848.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83466 MW;
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60.0%;
                                                                                                                      76.4%;
70.0%;
                                                                                                                                                                                               7; Conservative
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                                                                                                                                                                                                                                                                                                                                             877 EQWVEFIELN 886
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                                                                                                                                                                                                                                                                        1 DSWVEFIELD 10
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                                              1409 AA;
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Best Local Similarity
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Best Local Similarity
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BINDING
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Matches
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                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OTN-203 (Rel. 42, Last annotation update)
Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
(VEGFR-3) (Tyrosine-protein kinase receptor FLT4).
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000001; Prot. Kinase; 2.
SMART; SM0408; IGc2; 2.
SMART; SM00219; TYKc; 1.
PROSITE; PS50815; IG LIKE; 5.
PROSITE; PS50010; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50010; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
Transferase; Tyrosine-protein Kinase; Phosphorylation; ATP-binding; Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat; SIGNAL 1.
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
SIMILARITY: Belongs to the Tyr family of protein kinases.
CSF-1/PDGF receptor subfamily.
SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
       ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J;
MEDLINE=9330572; PubMed=8393164;
Finnerty H., Kelleher K., Morris G.E., Bean K., Merberg D. Kriz R., Morris J.C., Sookdeo H., Turner K.J., Wood C.R.;
"Molecular cloning of murine FLT and FLT4.";
Oncogene 8:2293-2298(1993).
       Indels
       7
                                                                                                                                                                                                       PRT; 1363 AA.
  Mismatches
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MGD, MGI:95561; Flt4.

GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR007110; Ig-like.
InterPro; IPR001824; Recepttyrkinsil.
InterPro; IPR001824; Recepttyrkinsil.
InterPro; IPR001824; Recepttyrkinsil.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Ffam; PF00047; ig; 5.
Pfam; PF00069; pkinase.il.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L07296; AAA40077.1; -. PIR; I58375; I58375.
  6; Conservative
                                                                                                                                                                                                     STANDARD;
                                                                                      544 DNWMKFFELD 553
                                            1 DSWVEFIELD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10090;
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                                                                                                                                                                                                     VGR3 MOUSE
P35917;
Matches
                                                                                                                                                      RESULT 13
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SIMILARITY).
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
VASCULAR ENDOTHELIAL GROWTH FACTOR
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MW; F1BF8A2BDEF99BE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
               RECEPTOR 3.
EXTRACELLULAR (POTENTIAL)
                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AUTO-)
                                                                                            IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 7.
IG-LIKE C3-TYPE 3.
IG-LIKE C3-TYPE 4.
IG-LIKE C3-TYPE 5.
IG-LIKE C3-TYPE 7.
IG-LIKE 7.
IG-LIKE 7.
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IG-L
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Signal recognition particle 9 kDa protein (SRP9).
SRP9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (1)
N-LINKED (GLUNAC, N-LINKED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC.
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(GLCNAC.
(GLCNAC.
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Pred. No. 20;
1; Mismatches
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527
582
594
683
690
758
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758 75
1363 AA;
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699
1068
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TIGR; S00213;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22297686; PubMed=12368813; Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Mean J.A., Schadari R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Muller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 1.1.1.158) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Biotechnol. 20:1118-1123 (2002).
-!- FUNCTION: Cell wall formation (By similarity).
-!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-acetyl-3-0-(1-carboxyvinyl)-D-glucosamine + NADPH.
-!- COFACTOR: FAD (By similarity).
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
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0
                                                                                                                                                                                                                                                                                                                                                                          Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                   B6EF4A9DA77C13BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                          69.1%; Score 38; DB 1; 75.0%; Pred. No. 3; iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylenolpyruvoylglucosamine reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 AA
                                                                                                                                                                                                                                                                        InterPro; IFROUSE, SRP9; 1.
Pfam; PF05486; SRP9; 1.
Signal recognition particle; RNA-binding.
                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                   EMBL; Y10117; CAA71203.1; -. PIR; T03951; T03951. HSSP; P49962; 1914. InterPro; IPR008832; SRP9. InterPro; IPR009018; SRP9/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acetylmuramate dehydrogenase)
MURB OR S00213.
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 DSWEEFVE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DSWVEFIE 8
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBEKBS;
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Gaps
           HAMAP; MF_00037; -; 1.
InterPro; IPR00317; -; 1.
InterPro; IPR0041004; Oxid FAD bind.
Pfam; PF01565; FAD binding_4; 1.
Pfam; PF01573; MAME C; 1.
IIGREPMS; TIGR00179; mAME; 1.
Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
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                                                                                                                          Peptidoglycan synthesis; Complete proteome.
SEQUENCE 341 AA; 37278 MW; FAE630BA722A3073 CRC64;
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Best Local Similarity 62.5
Best Local Si Conservative
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137 WVEYLDLD 144
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US-09-660-302D-3 55 1 DSWVEFIELD 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_25:*

1: Sp archea:*
2: Sp_bacteria:*
3: Sp fung:*
4: Sp human:*
5: Sp invertebrate:*
5: Sp mammal:*
5: Sp mammal:*
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sp_virus:*
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sp_unclassified:*
sp_rvirus:*
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105 AA.

PRT;

PRELIMINARY;

RESULT 2 Q863Q6 ID Q863Q6

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SEQUENCE FROM N.A.

KROEPELL K.-P., Wayne R.K.;

KrOEPELL K.-P., Wayne B.K.;

Type-1 STS Markers Are More Informative Than Cytochrome b in

Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";

Syst. Biol. 0:0-0(2003).

EMBL; AF4048191; AAP19682.1; -.

GO, GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                             Koepfii K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBI, AF498190; AAP19681.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lutra maculicollis (Spotted necked otter).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Rissipedia; Mustelidae; Lutrinae;
                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Pissipedia, Mustelidae, Lutrinae,
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106 106
106 AA; 12006 MW; EFBOCGDB793AE9FF CRC64;
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01-0UN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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                                                                                        Lutra lutra (European river otter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth hormone receptor (Fragment)
01-JUN-2003 (TrEMBLrel. 24, Create 01-JUN-2003 (TrEMBLrel. 24, Last s 01-CT-2003 (TrEMBLrel. 25, Last a Growth hormone receptor (Fragment)
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Koepfil K.-P., Rayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
                                                                                                                                                                                                                                       Koepflik.-P. Wayne R.K.;

"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).

EMBL: AF498187; AAP19678.1; -.

GO: GO:0004872; F:receptor activity; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae;
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105
105 AA; 11879 MW; F6F6445250DB79BF CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
                                                                                                                 Lontra canadensis (River otter) (Lutra canadensia).
                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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EMBL; AF498199; AAP19690.1; -.
GO; GO:0004872; F:receptor activity; IEA
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Matches 10; Conservative
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nes 10; Conserv
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Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498186; AAP19677.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498188; AAP19679.1;
GO:0004872; F:receptor activity; IEA.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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ive 0; Mismatches 0; Indels
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107 107
107 AA; 12151 MW; 84DD579D3C2EA9FE CRC64;
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           01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Growth hormone receptor (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                           Enhydra lutris (Sea otter)
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q863Q4
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL, AF498184; AAP19675.1; -.
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498185; AAP19676.1;
GO; GO:0004872; F:receptor activity; IEA.
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Lutrinae,
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107 107
107 AA; 12121 MW; 84DD579D3C2EB8BA CRC64;
01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Growth hormone receptor (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
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                                                                                                               Aonyx capensis (Cape clawless otter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth hormone receptor (Fragment).
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Koepfil K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498193; AAP19684.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
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Best Local Similarity 100.
Marches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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             Mustela erminea (Ermine)
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
EMBL; AF498192; AAP19683.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                    Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
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Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
                                     Loutra longicaudis (Neotropical otter) (Lutra longicaudis).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Carnivora, Rissipedia, Mustelidae, Lutrinae;
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107 AA; 12166 MW; 9113E14645IEA8BB CRC64;
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01-UJN-2003 (TrEMBLrel. 24, Created)
01-UJN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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EMBL; AF498189; AAP19680.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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  Growth hormone receptor (Fragment).
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Best Local Similarity 100.
Matches 10; Conservative
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"Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
Syst. Biol. 0:0-0(2003).
BMBL; AF498134; AAP19685.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
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100.0%; Score 55; DB 6; Length 107; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
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12140 MW; 96DBD146450149FE CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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                                                                               Koepfli K.-P., Wayne R.K.;
"Type-1 STS Markers Are More Informative Than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora)."; Syst. Biol. 0:0-0(22003).
EMBL; AF498195; AAP19686.1; ...
GO: GO: 0004872; F: receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Mustela vison (American mink).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Mustelidae, Mustelinae,
                                                                                                                                                                                                                                                                                                                                                                                                            GHR.
Martes americana (American marten)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
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                                                                                                                                                                                                           Query Match 100.0%; Score 55; DB 6; Length 107; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 10; Conservative 0; Mismatches 0; Indels
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107 107
107 AA; 12149 MW; 96CCE146450149FE CRC64;
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01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Growth hormone receptor (Fragment).
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                                                                      SEQUENCE FROM N.A.
                                              NCBI_TaxID=9667;
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NCBI_TaxID=9660;
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Q863P7
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Gaps

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Best Local Similarity 100. Matches 10; Conservative

δ g Search completed: June 9, 2004, 15:51:22 Job time : 33.5135 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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June Run on:

9, 2004, 15:36:10 ; Search time 35 Seconds (without alignments) 56.510 Million cell updates/sec

US-09-660-302D-7 1 CEEDFYR 7 score: Sequence: Title: Perfect

Scoring table:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
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geneseqp2003as:*
geneseqp2003as:* A_Geneseq_29Jan04:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query				
No.	нe		Le	DB	ΩI	Description
-	 	100.0	7	5	AAY32791	Aav32791 Pro
7	38	88.4	6	S	ABG94867	Abg94867 Hum
m	38	88.4	6	7	ADE82293	
4	38	88.4	33	7	AAR22456	Aar22456 Dla
S	38	88.4	246	7	AAR56389	
9	38	88.4	249	~	AAR06867	
7	38	88.4	269	7	AAR05045	Aarosous,
80	38	88.4	269	7	AAW10426	
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Description	Aava2741 Droteolyt	129	. 6	9	389 Human gr	67 Hormon	45	56	67 Human	02 Human	29 Solubl	52 Plasmid	9 Human fu	96 Human	08 Human	6 Human	94 Human				79 Protei	32	17 A. Cani	1701 Aca	93
SUMMARIES	AAY32791	ABG94867	ADE82293	AAR22456	AAR56389	AAR06867	AAR05045	AAW10426	AAY31767	AAW82802	AAY78429	ADE82252	AAU75499	AAU75496	AAP92108	AAP81326	AAW33394	ADD45067	ADD45063	ABB11437	ABU33279	AAY30432	AAB15317	AAR91701	AAY30393
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* or ™a	100.0	88.4	88.4	œ	∞.	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	88.4	æ	ė.	m.		83.7	83.7
Score	43	38	38	38	38	38	38	38	38	38	38	38	38		38	38	38	38	38	38	37	36	36	36	36
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Aay30454 Nematode Aab15346 A. caninu Aaw54077 LH-2 prot	Aab95251 Human pro Ade60425 Human Pro				Abp30/09 Streptoco Abu23159 Protein e	Add48732 Rat Prote Abq07365 Novel hum	Aau00294 Interfero Aam18331 Pentide #		Aam30819 Peptide # Abb32113 Peptide #
AAY30454 AAB15346 AAW54077	AAB95251 ADE60425 ADD45850	ADE60421 AAW54078	ABU47220	AAO11680	ABU23159	ADD48732 ABG07365	AAU00294 AAM18331	ABB37365	AAM30819 ABB32113
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26 27 28	30 10 10	32 33	3 4 35	36	38	39 40	41 42	43	44 45

ALIGNMENTS

RESULT 1

AAY32791 standard; peptide; 7 AA.

AAY32791;

(first entry) 09-NOV-1999

Proteolytic cleavage signal site used in inhibiting receptor proteolysis.

Signal transduction, proteolytic cleavage; cleavage signal site; ubiquitin; proteosome binding site; muscle wasting; renal tubular defect; uraemia; diabetes; Cushing's disease; eating disorder; AIDS; growth hormone deficiency.

Mammalia.

EP943624-A1

22-SEP-1999

98EP-00200799. 12-MAR-1998; 98EP-00200799. 12-MAR-1998;

(UYUT-) RIJKSUNIV UTRECHT.

WPI; 1999-510568/43.

Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

Claim 15; Page 27; 36pp; English.

This sequence is a cleavage signal site. This site is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage of the receptors being present on the proteolytic cleavage results in the receptors being present on the proteolytic cleavage results in the receptors being present on the the cell. This increases the sensitivity of cells to any hormones which might be present. The inhibitor is derived from or competes with an amino acid sequence around this proteolytic cleavage signal. The inhibitor may be used to treat muscle watting, associated with disorders such as renal tubular defects, uraemia, diabates, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease

Sequence 7 AA;

active domain in hGH. The method is useful for determining the relationship between structure and function of known polypeptide sequences. The present sequence shows a mutated part of an hGH binding protein, a target polypeptide for hGH used to test the binding of substitution mutants in the method of the invention

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Gaps

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Indels Length 9;

88.4%; Score 38; DB 5; Le 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;

6; Conservative

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Local Similarity

Query Match Matches

Sequence 9 AA;

88333333

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The invention relates to identifying an unknown active domain in a region of known amino acid sequence in a parent polypeptide e.g. human growth hormone (hGH) which has been cloned and has a pre-identified biological activity, where the active domain interacts with a target when the parent polypeptide is in its native-folded form and the interaction is comparable for the biological activity comprising: (a) comparing the amino acid sequence of polypeptide structure in the region of known amino acid sequence of hGH with the amino acid sequence or polypeptide structure in a region of known amino acid sequence or polypeptide comparable for a nanogue by parental lactogen or portine growth convenients at least 15% homology with hGH alpha-carbon coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates coordinates with the target is different from target interaction with hGH; (b) substituted bolypeptide; (c) contacting the segment from the analogue into DNA encoding the full length segment-substituted canalogue into DNA encoding the full length segment-substituted canalogue into DNA encoding the full length segment-substituted comparing the difference between activity of the first and second segment comparing the difference between activity of the lirst and second segment substituted polypeptides as an indication of the unknown cubstituted polypeptides as an indication of the unknown
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                                                                                                                                                                                                                                                                                                                                                                  Growth hormone; placental lactogen; prolactin; active domain; hGH; human; structure-function relationship; pJ1446; somatogenic receptor; segment-substituted polypeptide; hGH binding protein; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying active domains within cloned polypeptides of known amino sequence by substituting analog segments into the parent polypeptide useful to determine the relationship between structure and function.
                                        Gaps
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                                                                                                                                                                                                                                                                                                                               Human hGH binding protein carboxy terminus from pbGHr(1-246).
100.0%; Score 43; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06;
                                      0; Indels
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Col 31-32; 86pp; English
                                                                                                                                                                                                                 ABG94867 standard; peptide; 9 AA.
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92US-00875204.
92US-00960227.
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                                        Conservative
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  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                      CEEDFYR 7
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                                                                              1 CEEDFYR
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26-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                         ABG94867;
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human growth hormone; hGH; variant; somatogenic receptor.

plasmid phGhr (1-246) carboxy peptide fragment.

(first entry)

29-JAN-2004

ADE82293;

ADE82293 standard; peptide; 9 AA.

RESULT 3 ADE82293

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This invention describes a method for generating a novel human growth hormone (hGH) variant that binds to a target for hGH with an affinity different from affinity of wild type hGH for the target. Human growth hormone (hGH) has a positive binding activity with the target receptor. The human prolactin (hPRL), human placental lactogen (hHz) and portine growth hormone (hGH) nanlogues, however, have a greatly reduced activity with that target. Six segment-substituted growth hormones were formed by substituting selected amino acid segments of hGH with an analogues amino acid segment from the analogue. Bach of hese selected segments are different and were chosen to probe either the entire amino acid segmence of the hGH molecule or those regions which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Forming human growth hormone (hGH) variants by substitution mutation so that the variant binds to a target for hGH, e.g. hGH receptors or human prolactin receptors with affinity different from that of wild-type hGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expected to contain the active domains. This sequence represents a fragment of plasmid phGHz used in the generation of hGH binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Col 31-32; 87pp; English.
                                                                                                                                                                                                                                                          88US-00264611.
89US-00428066.
92US-00875204.
                                                                                                                                                                                                                                                                                                             92US-00960227
94US-00190723
                                                                                                                                                                                                                            95US-00486474
                                                                                                                                                                                                                                                                                                                                                                                            Cunningham BC;
                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-101735/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADE82294.
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                                                                                                                                                              US6451561-B1
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                                                                                                                                                                                                                                                                                                                             02-FEB-1994;
                                                                                                                               Synthetic.
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RESULT 4

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Extracellular C-domain protein of growth hormone receptor (hGHR-CD) - is used to enhance growth hormone function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The extracellular C-domain of hGHR is used to enhance growth hormone function. Two forms, Mel130Q-238Q (AAQ66550) and GS129V-238Q (AAQ66553) are given. Primers for the isolation of extracellular hGHR-CD are given in AAQ66551-52 and AAQ66554-55
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25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 9-10; 16pp; Japanese.
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                                                                                                                                                                                                                                                                                                                      (TANP-) TANPAKU KOGAKU KENKYUSHO
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                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant plasmid and Baculovirus having specific DNA fragment -used for prepn. of hormone binding region protein of human growth hormone
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 33; 3.3;
                                                                                 0; Indels
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                             88.4%; Score 38; DB 7; Length 9; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid pacYMhGHR; hGHR binding region; hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pBSR8-3 encoded polypeptide.
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                                                                                                                                                                                                                                                                                                                 AAR22456 standard; protein; 33 AA.
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                                88.4%;
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Query Match
Best Local Similarity 100.00
There 6; Conservative
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N-PSDB; AAQ23311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant;
human growth
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Matches

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Gaps

Matches

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RESULT 7 AAR05045

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A polypeptide (AAW10426) comprises the soluble extracellular domain of human liver growth hormone receptor (somatogenic receptor, shGHr). It was expressed in Escherichia coli transformants using a vector derived from pJ1446 (AAY1449). shGHr can be used in a novel method designed for the identification of polypeptide active domains. For human growth hormone segments of hGH with analogous segments from analogue selected amino acid segments of hGH with analogous segments from analogue polypeptides (human placenta lactogen, human prolactin and pig growth hormone) and examining placents are detd., active site amino residues (see also AAW10427-62) can be similarly identified. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of unknown active domains in polypeptide(s) - useful for analysis of structure and function of hormones, etc.
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                                              Active site; active domain; growth hormone; somatogenic receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 269; 27;
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               Human somatogenic receptor extracellular domain.
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100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                                               Human soluble growth hormone receptor.
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                                                                                                                                                1. .23
/label=_Sig_peptide
                                                                                                                                Location/Qualifiers
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92US-00875204.
92US-00960227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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N-PSDB; AAT10426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cunningham BC,
                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                               02-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                28-OCT-1988;
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                                                                 mutagenesis
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                                                                                                                                                                                                                                                                                                                                                                Plasmid pJ1446; human growth hormone; somatogenic receptor; mutagenesis; substitutions; active domain; hormone variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying active domains and aminoacid(s) in polypeptide(s) - by specific substitutions, then testing modified products for interaction with target, and new polypeptide, esp. hormone etc.
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                               88.4%; Score 38; DB 2; Length 249; 100.0%; Pred. No. 25; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                               Soluble human growth hormone receptor.
                                                                                                                                                                                                                AAR05045 standard; protein; 269 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW10426 standard; protein; 269 AA.
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(first entry)
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(first entry)
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                                                                 Conservative
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 AA;
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Sequence 249
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11-AUG-1997
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03-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Gaps

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Best Loc Matches

à αq RESULT 8

Homo sapiens

Peptide Protein 26-OCT-1989; 27-APR-1992; 13-OCT-1992;

28-OCT-1988

02-FEB-1994;

07-JUN-1995;

US5955346-A. 21-SEP-1999

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This is the amino acid sequence of human liver soluble somatogenic receptor, as encoded by a DNA insert of plasmid pul446 (see AAV62766). The livention provides methods for the systematic analysis of the structure and function of polypeptides by identifying active domains which influence the activity of the polypeptide with a target substance (for human growth hormone (see AAW82801, the target used was somatogenic receptor). Active domains are determined by substituting selected amino acid segments of the polypeptide with an analogous polypeptide segment, and comparing the activity of the substituted polypeptide with that of the mative polypeptide for the target. The invention also provides methods for identifying the active amino acids within the active domain. The method is particularly applied to hormones. Polypeptides can be properties than wild-type proteins, e.g. human growth hormone with increased potency but reduced diabetogenic activity and human prolactin or properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying amino acids in polypeptide(s) that are involved in interaction with target - by introducing scanning amino acid substitutions at selected positions and screening for any change in interaction, particularly to engineer hormones with altered properties.
1. .23
/label= Sig_peptide
                                   24. .269 //label= Mat_protein
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89US-00428066.
92US-00875204.
92US-00190727.
94US-00190727.
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26-OCT-1989;
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02-FEB-1994
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                                       Protein
   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a human soluble growth hormone receptor (shGHR) encoded by plasmid pJ1446 (see AAX87977). shGHR was expressed in E. coli and was used in blinding assays of human growth hormone variants. The invention provides a method for the systematic analysis of the structure and function of polypeptides by identifying active domains which influence the activity of the polypeptide with a target substance, and method for identifying the active amino acid residues within the active domain of a polypeptide. It also provides polypeptide variants comprising segment-substituted and residue-substituted growth hormones, prolactins (see AAX11764) and placental lactogens (see AAX11765). Identifying receptor binding sites in hormones permits the rational design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids encoding variants of human prolactin and placental lactogen useful for identifying active domains within those proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Somatogenic receptor; growth hormone; human; plasmid p11446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.4%; Scor.
100.0%; Pred. No. ...
                                                                      1. .23
/note= "signal peptide"
                                                                                                         24. .269 _ _ _ _ /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 12A-C; 86pp; English.
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human soluble somatogenic receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW82802 standard; protein; 269 AA
                                                                                                                                                                                                                                                                           88US-00264611.
89US-00428066.
92US-00875204.
                                                                                                                                                                                                                                            95US-00476999
                                                                                                                                                                                                                                                                                                                                    92US-00960227
                                                                                                                                                                                                                                                                                                                                                      94US-00190723
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                                                                                                                                                                                                                                                                                                                                                                                                                                Wells JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-560495/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||
264 CEEDFY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAX87977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CEEDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                Cunningham BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         active domain.
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o;
                                                                                                                                                                                                                                                                                                                                                                                Human growth hormone; hGH; prolactin; placental lactogen; modification;
                                                                                                                                                                                                                                                                                                                                       Soluble part of the somatogenic receptor encoded by plasmid pJ1446.
                                         0;
DB 2; Length 269; 27;
                                       Indels
                                       ;
0
                                         Mismatches
88.4%; Score 38;
100.0%; Pred. No.
                                                                                                                                                                                                                    AAY78429 standard; protein; 269 AA.
                  Similarity 100.0%; Pr
6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                     mutagenesis.
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Location/Qualifiers

Homo sapiens.

01-MAR-1999

AAW82802;

Query Match

Matches

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Forming human growth hormone (hGH) variants by substitution mutation so that the variant binds to a target for hGH, e.g. hGH receptors or human prolactin receptors with affinity different from that of wild-type hGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 12A-C; 87pp; English.
                                                                                                        88US-00264611.
89US-00428066.
92US-00875204.
92US-00960227.
94US-00190723.
                                                               95US-00486474
                                                                                                                                                                                                                                                                                           Cunningham BC;
                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                      WPI; 2003-101735/09.
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADE82251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CEEDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAY-2002
                                                               07-JUN-1995;
                                                                                                                                                                                                    02-FEB-1994;
                                                                                                                                    26-OCT-1989;
                                                                                                                                                       27-APR-1992;
                                                                                                                                                                              .3-OCT-1992;
                                                                                                            28-OCT-1988;
                  17-SEP-2002
                                                                                                                                                                                                                                                                                           Wells JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU75499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU75499
%XCCCCCCCCCCX%X4444X8X4X4X8XX8XX8XX8XX8X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes the production of a polypeptide variant (I) comprising segment substituted and residue substituted growth hormone, prolactin or placental lactogens. The method is particularly used to produce variants of growth hormone (GH), prolactin or placental lactogens, the method is particularly classed to produce variants of growth hormone (GH), prolactin or placental lactogen, but may also be applied to receptors, interferons, and colonyclation is the production of human GH variants with altered (decreased or increased) binding interaction with the somatogenic receptor, i.e. compounds useful as human GH variants and which may have higher potency for stimulating other human GH receptors, and as standards or tracers in immunoassays for human GH. This method of DNA selection identifies the biologically active residues in active domains, including those critical for interaction with different targets. The present sequence represents the soluble region of the somatogenic receptor from liver encoded by a plasmid, which is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant production of variant polypeptides, e.g. growth hormone variants with altered receptor specificity, using cells transformed with DNA selected by scanning mutagenesis in at least one peptide domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human growth hormone; hGH; variant; somatogenic receptor; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.4%; Score 38; DB 3; Length 269; 100.0%; Pred. No. 27; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pBJ1446 containing growth hormone (hGH) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE82252 standard; protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 12; 83pp; English
                                                                                                                                                                                                                    88US-00264611.
89US-00428066.
92US-00875204.
92US-001960227.
94US-001960227.
                                                                                                                                                                            98US-00104036
                                                                                                                                                                                                                                                                                                                                                             97US-00903398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wells JA, Cunningham BC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-159873/14.
N-PSDB; AAZ88448.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CEEDFY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 269 AA;
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                                                                                                                                                                              24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                             30-JUN-1997;
                                                                                                                                                                                                                                              26-OCT-1989;
27-APR-1992;
                                                                                                                                                                                                                                                                                           13-OCT-1992;
                                                                                                                                                                                                                                                                                                                 02-FEB-1994;
                                                                                       US6013478-A.
                                                                                                                                  11-JAN-2000
                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE82252;
                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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à
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This invention describes a method for generating a novel human growth hormone (hGH) variant that binds to a target for hGH with an affinity different from affinity of wild type hGH for the target. Human growth hormone (hGH) has a positive binding activity with the target receptor, the somatogenic receptor. The human prolactin (hPRL), human placental lactogen (hFL) and porcine growth hormone (pGH) analogues, however, have a greatly reduced activity with that target. Six segment-substituted agreatly reduced activity with that target. Six segment-substituted growth hormones were formed by substituting selected amino acid segments of hGH with an analogous amino acid segment from the analogue. Each of these selected segments are different and were chosen to probe either the expected to contain the active domains. This sequence represents the plasmid pyll466 which contains the synthetic hGH described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; GHS1-23; human growth hormone; GH; GHR; growth hormone; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHStopGHR SD100; GHlinkGHR; GHlinkGHRflec; pTrcRNSsacI; TrcHindrev; Chi 1A2 chimaera; acromegaly; gigantism; growth hormone deficiency; Turner's syndrome; renal failure; osteoporosis; diabetes mellitus; cancer; obesity; insulin resistance; hyperlipidaemia; hypertension; anaemia; autoimmune disease; infectious disease; inflammatory disorder; rheumatoid arthritis; interleukin-6 chimaera; IL-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.4%; Score 38; DB 7; Length 269; 100.0%; Pred. No. 27; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU75499 standard; protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human fusion protein Chi 1A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 CEEDFY 269
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Human fusion protein GHlinkGHR.

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The invention relates to a binding agent comprising a first part capable of binding a ligand binding domain of a receptor linked to a second part comprising a receptor binding domain, where the binding agent modulates the activity of the receptor. Also included are a nucleic acid molecule having a sequence, which encodes a binding agent comprising sequences of a paven in the specification comprising the sequences of the full length GHStopGHR SD100 construct, GHIINGGHR construct, GH, growth hormone receptor, GHIINGGHR construct, 1157 base pair PCR fragment GHIINGGHR generated by nucleotides pTrcRNSac1 and TreHindrev, or the nucleotide sequence of the Chi 1A2 chimaera, sequences binding to the nucleic acids or degenerate sequences representing them (which have receptor antagonising activity), their encoded polypeptides, a vector comprising the nucleic acids and a cell transformed/transfected with the nucleic acid or vector. The binding agent is useful for manufacturing a medicament for the treatment of acromegaly, gigantism, growth hormone (GH) deficiency, Turner's syndrome, renal failure, osteoporosis, diabetes mellitus, cancer, obesity, insulin resistance, hyperlipidaemia, (IL)-6 hypertension, anaemia, autoimmune and infectious diseases, and inflammarcry disorders including rheumatoid archritis (interleukin (IL)-6 chimaera). The present sequence represents the fusion protein agent of the invention being the Chil 1A2 conserts the fusion protein agent of the invention being the Chil 1A2 conserts the perfect of peptide linker)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New binding agent useful in producing a medicament for treating e.g. cancer, obssity, acromegaly or gigantism, comprises a first part that binds to a ligand binding domain of a receptor and a second part having receptor binding domain.
                                                                                           /label= Unknown
/note= "Encoded by TAA, in-frame stop codon"
                                                   /note= "Encoded by TGA, in-frame stop codon"
Misc-difference 312
/label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 49; Fig 22; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sayers J;
                                                                                                                                                                                                                                                                                      2000GB-00014765.
2001GB-00005969.
2001GB-00006487.
                                                                                                                                                                                                                                            18-JUN-2001; 2001WO-GB002645
                                                                                                                                                                                                                                                                                                                                                                                                                   Artymiuk P,
                                                                                                                                                                                                                                                                                                                                                                         (ASTE-) ASTERION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-130734/17
                                                                         Misc-difference 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK14547
                                                                                                                                                            WO200196565-A2
                                                                                                                                                                                                                                                                                      16-JUN-2000;
10-MAR-2001;
                                                                                                                                                                                                                                                                                                                                 16-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Ross R,
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0;
5; Length 315;
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Gaps
                            ·.
                           0; Indels
88.4%; Scor.
100.0%; Pred. No. 52,
... 0; Mismatches
                          6; Conservative
                                                             CEEDFY 311
                Best Local Similarity
                                            1 CEEDFY 6
                                                               306
       Query Match
                          Matches
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(first entry)
                                               08-MAY-2002
                               AAU75496;
RESULT 14
AAU75496
ID AAU7
XX
AC AAU7
XX
DT 08-M
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AAU75496 standard; protein; 340 AA.

DB 5;

88.4%; Score 38;

Query Match

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The invention relates to a binding agent comprising a first part capable of binding a ligand binding domain of a receptor linked to a second part comprising a receptor binding domain, where the binding agent modulates the activity of the receptor. Also included are a nucleic acid molecule having a sequence, which encodes a binding agent comprising sequences given in the specification comprising the sequences of the full length growth hormone receptor, GHlinkGHR construct, 1157 base pair PCR fragment GHlinkGHR generated by nucleotides pTrcRNSsacI and TrcHindrev, or the nucleotide sequence of the Chi 1A2 chimaera, sequences binding to the nucleic acids or degenerate sequences representing them (which have receptor antagonising activity), their encoded polypeptides, a vector comprising the nucleic acids and a cell transformed/transfected with the nucleic acid or vector. The binding agent is useful for manufacturing a medicament for the treatment of accomegaly, gigantism, growth hormone (GH) the deficiency. Turner's syndrome, renal failure, osteoporois, diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New binding agent useful in producing a medicament for treating e.g. cancer, obesity, acromegaly or gigantism, comprises a first part that binds to a ligand binding domain of a receptor and a second part having a receptor binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension, anaemia, autoimmune and infectious diseases, and inflammatory disorders including rheumatoid arthritis (interleukin (IL)-6 chimaera). The present sequence represents the fusion protein agent of the invention being the GHlinKGHR construct (growth hormone/growth hormone receptor linked by a synthetic peptide linker)
                                Human; GHS1-23; human growth hormone; GH; GHR; growth hormone; receptor; GHsropGHR SD100; GHlinkGHR; GHlinkGHRflec; pTrcRNSsac1; TrcHindrev; Chi 1A2 chimaera: acromegaly; gigantism; growth hormone deficiency; Turner's syndrome; renal failure; osteoporosis; diabetes mellitus; cancer; obesity; insulin resistance; hyperlipidaemia; hypertension;
                                                                                                                                          anaemia; autoimmune disease; infectious disease; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mellitus, cancer, obesity, insulin resistance, hyperlipidaemia,
                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by TGA, in-frame stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                              /label= Unknown
/note= "Encoded by TAA, in-frame stop codon"
                                                                                                                                                              rheumatoid arthritis; interleukin-6 chimaera; IL-6.
                                                                                                                                                                                                                                                                                                        'note= "Encoded by ATG"
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 6; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                    /label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-2001; 2001GB-00005969.
16-MAR-2001; 2001GB-00006487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-2000; 2000GB-00014765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUN-2001; 2001WO-GB002645
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                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 338
                                                                                                                                                                                                                                                                                                                              Misc-difference 33
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                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An animal can be immunised against its growth hormone receptor by vaccinating against a growth hormone receptor extracellular domain deriv. predetermined to raise polyclonal antisera which affect the receptor as a growth hormone against. This method enables continuous growth of target tissues without frequent hormone admin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modulating growth hormone receptor activity - by immunising animal against growth hormone receptor extracellular domain deriv. to raise
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                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI;
           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Martin DW, Spencer SA,
100.0%; Pred. No. 35; rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2a-c; 18pp; English.
                                                                                                                        AAP92108 standard; protein; 637 AA.
                                                                                                                                                                                                  Human growth hormone receptor.
                                                                                                                                                                                                                                                                                                                         87US-00061942.
                                                                                                                                                                                                                                                                                                                                               85US-00737302.
86US-00861236.
                                                                                                                                                                         14-FEB-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                        Growth hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                              Hammonds RG, Leung DW,
                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-300419/41.
N-PSDB; AAN91325.
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                                                   331 CEEDFY 336
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                                    1 CEEDFY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 637 AA;
                                                                                                                                                                                                                                                                                                                                                 22-MAY-1985;
07-MAY-1986;
                                                                                                                                                                                                                                                                                                                         12-JUN-1987;
                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                 AAP92108;
                                                                                               RESULT 15
                                                                                                              AAP92108
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Search completed: June 9, 2004, 15:48:28 Job time : 36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 9, 2004, 15:43:40; Search time 7.75676 Seconds (without alignments) 86.807 Million cell updates/sec Run on:

US-09-660-302D-7 1 CEEDFYR 7 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		a k e			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
-		00	638	7	A33991	somatotropin recep
7		83.7	364	Н	TVHUML	
£,	36	83.7	368	1	TVMSML	
ጥ		83.7	378	N	JC5658	
2		83.7	400	0	JC5657	LIM domain-contain
9		83.7	426	Н	A47179	homeotic protein L
7	36	83.7	726	(1	B86202	hypothetical prote
80	32	81.4	202	7	B81371	
6	35	81.4	552	7	AC0609	
10	35	81.4	1376		S63986	collagen alpha 5 c
11	35	81.4	1822		263985	a
12	35	81.4	3198		A43426	
13	34	79.1	277		E84478	hypothetical prote
14	34	79.1	331		E97111	L-asparaginase [im
15	34	79.1	563		AG2393	DNA repair helicas
16	34	79.1	599		A57701	sterol esterase (E
17		79.1	612	~	A34967	sterol esterase (E
18		79.1	625		T40742	hypothetical integ
19	34	79.1	707		A64047	ribonucleoside-tri
20	33	76.7	98		H69321	hypothetical prote
21	33	76.7	272	7	D90597	conserved hypothet
22	33	76.7	441		T28411	ORF MSV250 hypothe
23		76.7	496	7	T20926	hypothetical prote
24	32	74.4		7	B84973	н
25		74.4	200	7	T42678	hypothetical prote
56	32	74.4	309	7	T38671	
27	32	74.4	352	7	C85909	hypothetical prote
28	32	74.4	352	~	G91064	
29	32	74.4	395	Н	I50376)t

hypothetical prote	threonine dehydrat	histamine H1 recep	histamine H1 recep	histamine H1 recep	histamine H1 recep	hypothetical prote	netrin-2 precursor	netrin-1 precursor	transcription fact	probable ATP-depen	conserved hypothet	coatomer complex b	receptor-like tyro	receptor tyrosine	protein-tyrosine k
C86202	G83863	JC1415	JC2495	156507	A41632	G84710	B54665	A54665	\$26386	A81349	F71369	T39962	S51603	S47489	A36355
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407	415	486	487	488	491	531	581	909	647	929	740	196	893	868	916
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74.4	74	7	•												
32 74.4	32 74	32 7	32	32	32	32	32	32	32	32	32	32	32	32	32

ALIGNMENTS

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5	991
5	6

somatotropin receptor precursor - human

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-638 <GOD>

A,Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; GB:M28460; GB

A;Accession: S04530 A;Molecule type: mRNA A;Residues: 1-543,'I', 545-638 <LEU> A;Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738

C,Genetics: A,Gene: GDB:GHR

A; Cross-references: GDB:119984; OMIM:600946

A;Map position: 5p13-5p12 C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: liver; transmembrane protein C;Keywords: liver; transmembrane protein F;1-18/Domain: signal sequence #status predicted <SIG> F;19-638/Foduct: somatotropin receptor #status predicted <MAT> F;265-288/Domain: transmembrane #status predicted <TMM>

Query Match 88.4%; Score 38; DB 2; Length 638; Best Local Similarity 100.0%; Pred. No. 14; Matches 6; Conservative 0; Mismatches 0; Indels

0

Gaps

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ð g RESULT 2

transforming protein L-myc-1 - human C;Species: Homo sapiens (man) C;Date: 30-Sep-1989 #sequence revision 30-Sep-1989 #text_change 18-Jun-1999 C;Accession: A27675; S01200; \$09390 R;Kaye, F.; Battey, J.; Nau, M.; Brooks, B.; Seifter, E.; De Greve, J.; Birrer, M.; Saus Mol. Cell, Biol. B, 186-195, 1988

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C; Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 15-Oct-1999
C; Accession: JC5658
R; Nohno, T.; Kawakami, Y.; Wada, N.; Ishikawa, T.; Ohuchi, H.; Noji, S.
B; Ochem. Biophys. Res. Commun. 238, 506-511, 1997
A; Title: Differential expression of the two closely related LIM-class homeobox genes LH A; Reference number: JC5657; MUID: 97446014; PMID: 929541
A; Reference number: JC5657; MUID: 97446014; PMID: 929541
A; Accession: JC5658
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-378 cNOH3
A; Residues: 1-378 cNOH3
A; Residues: DNA
A; R
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Jul-1997
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Jul-1997
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Jul-1997
R;Xu, Y:; Baldassare, M:; Fisher, P:; Rathbun, G.; Oltz, E.M.; Yancopoulos, G.D.; Jesse Proc. Natl. Acad. Sci. U.S.A. 90, 227-231, 1993
A;Title: LH-2: a LIM/homeodomain gene expressed in developing lymphocytes and neural ce
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Pred. No. 21;
2; Mismatches 0; Indels
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71.4%;
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5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conserv
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                       а
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A;Cross-references: GB:M19720; NID:g188906; PIDN:AAA59879.1; PID:g386964
R;Cross-references: GB:M19720; NID:g188906; PIDN:AAA59879.1; PID:g386964
R;DePlinho, R.A.; Hatton, K.S.; Tesfaye, A.; Yancopoulos, G.D.; Alt, F.W.
Genes Dev. 1, 1311-1326, 1987
A;Title: The human myc gene family: structure and activity of L-myc and an L-myc pseudog A;Reference number: S01200; MUID:88112807; PMID:3322939
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R;Legouy, B.; DePinho, R.; Zimmerman, K.; Collum, R.; Yancopoulos, G.; Mitsock, L.; Kriz MsDo J. 6, 339-3366, 1987
A;Title: Structure and expression of the murine L-myc gene.
A;Reference number: S03017; MUID:88111523; PMID:2828024
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A;Molecule type: DNA
A;Residues: 1-368 cLEGs
A;Cross-references: GB:X13945; GB:X06183; GB:X13949; GB:Y00082; NID:g53287; PIDN:CAA3212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-364 < DRP>
R; Ikegaki, N.; Minna, J.; Kennett, R.H.
BMBO J. 8, 1793-1799, 1999, and L-myc gene is expressed as two forms of protein in small cell lung
A; Title: The human L-myc gene is expressed as two forms of protein in small cell lung
A; Reference number: S09390; MUID:89356654; PMID:2548855
                       A;Title: Structure and expression of the human L-myc gene reveal a complex pattern of A;Reference number: A27675; MUID:88094386; PMID:2827002
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:120706; OMIM:164850
A;Map position: 1p32-1p32
A;Introns: 166/1
C;Superfamily: myc transforming protein; myc transforming protein homology
C;Keywords: DNA binding; nucleus; transforming protein
F;1-364/Domain: myc transforming protein homology <MYC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 19;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 19;
0; Mismatches
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A;Molecule type: protein
A;Residues: 165-179 <IKE>
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Best Local Similarity
6; Conserve
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                               A; Molecule type: DNA
                                                                                                                A; Accession: A27675
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C;Accession: AC0609
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, h. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Cross-references: GB:AL139076, GB:AL111168; NID:96968128; PIDN:CAB73220.1; PID:g696840
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
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A;Cross-references: EMBL:X89804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein STY0935 [imported] - Salmonella enterica subsp. enterica S, Speciess: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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C;Superfamily: von Willebrand factor type C repeat homology
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A;Cross-references: GB:AL513382; PIDN:CAD05341.1; PID:g16502105; GSPDB:GN00176 C;Genetics:
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F;15-73/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                    Length 202;
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Pred. No. 45;
2; Mismatches
                                                                                                                                                                                                                    Score 35; DB
Pred. No. 17;
1; Mismatches
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A;Molecule type: DNA
A;Residues: 1-1376 <EXP>
A;Cross-references: EMBL:X89804
Sibmitted to the EMBL Data Library, July 1995
A;Reference number: S64637
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71.48;
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83.3%;
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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A; Status: preliminary
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                                                                                                                                                         A; Gene: Cj0963
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                                                    A;Reference number: A47179; MUID:93126348; PMID:7678338
A;Accession: A47179
A,Status: preliminary
A,Status: preliminary
A,Status: preliminary
A,Rolecule type: mRNA
A,Residues: 1-426 <XUI>
A,Cross-references GB:L06804
A,Experimental source: brain
A,Note: sequence extracted from NCB1 backbone (NCBIN:122101) (NCBIP:122102)
A,Rote: sequence extracted from NCB1 backbone (NCBIN:122101) (NCBIP:122102)
C;Superfamily: homeotic protein LH-2; homeobox, homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; homeobox, nucleus; transcription regulation; zinc F;S2-104/Domain: LIM metal-binding repeat homology <LIMI>
F;114-167/Domain: LIM metal-binding repeat homology <LIMI>
F;265-321/Domain: homeobox homology <HOX>
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C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Doll #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C'Accession: B86202
R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anthors: Hudbes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., J. J.H.; J.H.; Lin, X.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B86202
A;Accession: B86202
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A,Reference number: A81250; MUID:20150912; PMID:10688204
A,Accession: B81371
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hypochetical protein C10963 [imported] - Campylobacter jejuni (strain NCTC 11168)

C;Species Campylobacter jejuni
C;Date: 31-Mar-2000 #text_change 03-Jun-2002

C;Accession: B81371

E;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
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A;Map position: 1
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Pred. No.
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Best Local Similarity 85.7
Matches 6; Conservative
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101 CKEDYYR 107
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CEEDVYR 639
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A;Molecule type: DNA
A;Residues: 1-202 <PAR>
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hypothetical protein At2g06570 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84478
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A;Titles: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L'asparaginase [imported] - Clostridium acetobutylicum
C,Species: Clostridium acetobutylicum
C,Species: Clostridium acetobutylicum
C,Accession: E97111
R,Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
T, Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A,Accession: E97111
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG2393

Wh repair helicase [imported] - Nostoc sp. (strain PCC 7120)

C,Species: Nostoc sp. PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C,Date: 14-Dec-2001

R,Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

RNARZAKI, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

NARZAKI, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A,Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Residues: 1-331 <KUR>
A;Residues: 1-331 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79680.1; PID:g15024680; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-277 <STC>
A;Cross-references: GB:AE002093; NID:g4584359; PIDN:AAD25153.1; GSPDB:GN00139
C;Genetics:
C;Genetics:
A;Gene: A:2g06570
A;Map position: 2
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Pred. No. 36;
1; Mismatches
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Pred. No.
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100.0%; Pred
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83.3%;
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C,Superfamily: asparaginase
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Best Local Similarity
Matches 6; Conserv
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Matches 5; Conserv
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                                       RESULT 13
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A; Residues: 1-381, DT', 384-677, N', 679-1010, L', 1012-1822 <EXW>
A; Cross-references: EMBL: X89806
C; Genetics:
A; Gene: COLL2alpha
A; Introns: 33/1; 106/1; 169/2; 254/1; 395/1; 460/3; 534/1; 678/1; 743/3 817/1; 965/1; 11
F; 48-106/Domain: von Willebrand factor type C repeat homology <VWC>
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R;Exposito, J.Y.; D'Alessio, M.; Ramirez, F.
J. Biol. Chem. 267, 17404-17408, 1992
J. Biol. Chem. 267, 17404-17408, 1992
A;Title: Novel amino-treminal propeptide configuration in a fibrillar procollagen underga;Reference number: A43426, MUID:92381062; PMID:1380962
A;Recession: A43426
A;Reture: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 2 chain precursor - sea urchin (Strongylocentrotus purpuratus) (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 20-Unl-1996 #sequence_revision 01-Nov-1996 #text_change 15-Sep-2003
C;Date: 20-Unl-1996 #sequence_revision 01-Nov-1996 #text_change 15-Sep-2003
C;Accession: S63985; Sef637
Eur. J. Biochem. 234, 59-65, 1995
Eur. J. Biochem. 234, 59-65, 1995
A;Title: Characterization of two genes coding for a similar four-cysteine motif of the A;Reference number: S63985; MUID:96096722; PMID:8529669
A;Accession: S63985
A;Accession: S6398
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A; Residues: 1-3198 (EXP)
A; Residues: 1-3198 (EXP)
A; Cross-references: GB: M92041; NID: g161448; PIDN: AAA30040.1; PID: g161449
A; Note: sequence extracted from NCBI backbone (NCBIP: 111965)
F; 48-106/Domain: von Willebrand factor type C repeat homology <VWC>
F; 2978-3198/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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                                       Length 1376;
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Score 35; DB 2; Length 13,7
Pred. No. 1.1e+02;
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83.3%; Pred. No. 1.46+02;
ive 1; Mismatches 0; Indels
                                                                                                         1; Mismatches
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A;Reference number: S64637
A;Accession: S64637
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A,Accession: AG2393
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-563 «KUR»
A,Toros-references: GB:BA00019; PIDN:BAB76402.1; PID:g17133840; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: alr4703
                                                                                                                                                                                                                                                         Query Match
Post Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels
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Search completed: June 9, 2004, 15:52:18 Job time: 8.75676 secs

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GenCore version 5.1.6
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June 9, 2004, 15:36:55; Search time 5.10811 Seconds (without alignments) 71.355 Million cell updates/sec Run on:

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Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NET1_CHICK PEPO_LACHE SKO1_YEAST NETA_DROME COPP_SCHPO EPAZ_HUMAN EPAS_HUMAN PCK5_BRACL YHCO_ECOLI YHCO_ECOLI YER2_ARATH
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ALIGNMENTS

RESULT 1

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EMBO J. 13:1386-1395(1994)
                                       human genes.";
                                                         Subfamily
                                      Lander E.S.;
                                          ERRATUM.
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EMBL; M28466; AAA52555.1; -. EMBL; M28458; AAA52555.1; JOINED.

EMBL; X06562; CAA29808.1; -.

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PDB; 1A22; 29-APR-98.
PDB; 1XF9; 20-NOV-02.
Genew; HGNC;4263; GHR.
MIM; 600946; -..
                                                                                                                                           PIR, A33991, A33991.
PDB, 3HHR, 30-APR-94.
PDB, 1HWG, 19-NOV-97.
PDB, 1HWH, 19-NOV-97.
                                                                                                                                         A33991; A33991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                                       MEDLINE=96013502; PubMed=7565946; Goddard A.D., Covello R., Luoh S.-M., Clackson T., Attie K.M., Gesundheit N., Rundle A.C., Wells J.A., Carlsson L.M.S.; "Mutations of the growth hormone receptor in children with idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579. MEDLINE-99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.K., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Marrington J., Lipshutz R., Daley G.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [MIM:600946].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norstedt G.; Crystal structure of an antagonist mutant of human growth hormone, Gl20Rt, in complex with its receptor at 2.9-A resolution."; J. Biol. Chem. 271:32197-32203 (1996).
                    MEDLINE=94185645; PubMed=8137822;
Musquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R., Savage M.O., Preece M.A., Craescu C.T., Blouquit Y., Goossens M., Amselem S.;
                                                                                             "A single amino acid substitution in the exoplasmic domain of the human growth hormone (GH) receptor confers familial GH resistance (Laron syndrome) with positive GH-binding activity by abolishing receptor homodimerization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Vos A.M., Ultsch M., Kossiakoff A.A.; "Human growth hormone and extracellular domain of its receptor:
                                                                                                                                                                                                                                      VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Subfamily 1.
-!- SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.
MEDLINE=97113023; PubMed=8943276;
                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-256.
MEDLINE=92196577; PubMed=1549776;
                                                                                                                                                                                                                                                                                                                                                      short stature.";
New Engl. J. Med. 333:1093-1098(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crystal structure of the complex.". Science 255:306-312(1992).
VARIANT LARON DWARFISM HIS-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 23:373-373(1999).
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/FTId=VAR_002713.
R -> C (in Laron dwarfism and idiopathic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR 013938.
E -> D (in idiopathic short stature).
/FTId=VAR 002716.
C -> F (in dbSNP:6182).
/FTId=VAR 013939.
P -> T (in dbSNP:6183).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR 002709.
F -> S (in Laron dwarfism).
/ FTId=VAR 002710.
V -> A (in Laron dwarfism).
/ FTId=VAR 002711.
V -> D (in Laron dwarfism).
/ FTId=VAR 002712.
D -> H (in Laron dwarfism; abolish).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                           R GO: GO: 0005887; C: integral to plasma membrane; TAS.
R GO: GO: 0004903; F: growth hormone receptor activity; TAS.
R GO: GO: 0007150; F: growth hormone receptor activity; TAS.
R GO: GO: 0007150; P: growth pattern; TAS.
R GO: GO: 0001501; P: skeletal development; TAS.
R InterPro; IPR002996; CRIA.
R InterPro; IPR003961; FN III.
R Pfam; PR00041; ffa3; H=mtopoptn_L_FI.
R PART; SM0060; FN3; I.
R PROSITE; PS01352; HEMATOPO_REC_L_FI; I.
R RECEPTO; Transmembrane; GIycoprotein; Signal; 3D-structure; Marfism; Polymorphism; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_002714.

R -> H (in_dboNP:6181).
/FTId=VAR_01393.
R -> G (in_Laron dwarfism).
/FTId=VAR_002715.
R -> H (in_dboNP:6177).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E -> K (in idiopathic short
/FTId=VAR_002708.
R -> K (in Laron dwarfism).
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I -> L (in dbSNP:6180).
/FTId=VAR 013941.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    short stature)
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
        EMBL; M28460; AAA52555.1; JOINED.
EMBL; M28461; AAA52555.1; JOINED.
EMBL; M28462; AAA52555.1; JOINED.
EMBL; M28443; AAA52555.1; JOINED.
EMBL; M28464; AAA52555.1; JOINED.
EMBL; M28466; AAA52555.1; JOINED.
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259 CEEDFY 264

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RESULT 3
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97733601; PubMed=9228076;
Martini J.F., Pezet A., Guezennec C.Y., Edery M., Postel-Vinay M.C.,
Kelly P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Monkey growth hormone (GH) receptor gene expression. Evidence for
two mechanisms for the generation of the GH binding protein.";
J. Blol. Chem. 272:18951-18958 (1997)
-1- FUNCTION: This is a receptor for pituitary gland growth hormone.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                         Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                      ;
0
                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Growth hormone receptor precursor (GH receptor) (Serum binding
                    Score 38; DB 1; Length 638;
Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1; Length 638;
Pred. No. 8.1;
                                                    0; Indels
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InterPro; IPR002996; CRIA.

InterPro; IPR003961; FN III.

InterPro; IPR003528; Hemtopoptn_L_F1.

SMART; SM00060; FN3; 1.

PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

Receptor; Transmembrane; Glycoprotein; Signal.

18 POTENTIAL.

POTENTIAL.
                                                    Mismatches
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       88.4%; SC. 100.0%; Pre
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100.0%; Pre
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                                               Conservative
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Query Match
Best Local Similarity
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P79194;
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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=20069078; PubMed=10602999;
Lemmens I.H., Parnebo F., Piehl F., Merregaert J., Van de Ven W.J.M.,
Larsson C., Kas K.;
"Molecular characterization of human and murine cllorfs, a new member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of needles (N147) (Fragments).
Pinus pinaster (Maritime pine).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Coniferopsida, Coniferales, Pinasceae, Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Needle; MEDLINE=99274088; PubMed=10344291; MEDLINE=99274088; PubMed=10344291; Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomino C.; Rigerio J.-M., Plomino C.; Resparation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: On the 2-gel the determined pI of this unknown protein is: 5.6, its MM is: 36 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                 of the FAUNA gene cluster.";

Mamm. Genome 11:78-80(2000).

-!- TISSUE SPECIFICITY: Low expression in most tissues; highly expressed in testis; particularly in seminiferous tubules.
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Pred. No. 7.7;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43038 MW; 6BED852632747B54 CRC64;
                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein Cllorf5 homolog (Protein FON)
  399 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch}.
  PRT;
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                                            28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF119498; AAF23592.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1352481; ORF6.
InterPro; IPR007529; Znf_HIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.0%;
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04438; zf-HIT;
SEQUENCE 399 AA; 43(
                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=71647;
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MOUSE
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                                                                                                                                           C11ORF5
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CEEDFY 6

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Gaps

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0; Indels

Mismatches

Local Similarity 100. 1es 6; Conservative

Best Loca Matches

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InterPro; IPR002418; TF_Myc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                         Kaye F., Battey J., Nau M., Brooks B., Seifter E., de Greve J.,
Birrer M., Sausville E., Minna J.;
Structure and expression of the human L-myc gene reveal a complex
pattern of alternative mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                           MEDIJNE=88112807; PubMed=3322939; DePinho R.A., Hatton K.S., Tesfaye A., Yancopoulos G.D., Alt F.W., "The human myc gene family: structure and activity of L-myc and an
                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                            .
0
                                                                          Length 20;
                                                         9F4E4678E086C298 CRC64;
                                                                         Score 36; DB 1;
Pred. No. 0.51;
                                                                                                                                                                             MYCL HUMAN STANDARD; PRT; 364 AA. P12554; Q9NUB9; 01-0CT-1989 (Rel. 12, Created) 10-CT-1989 (Rel. 12, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
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지 . . 보.
지 . . 또
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                                                                                                                                                                                                                                                                                                    MEDLINE=88094386; PubMed=2827002;
                                                                                              2;
                                                                                                                                                                                                                            L-myc-1 proto-oncogene protein.
                                                                                                                                                                                                                                                                                                                                                                                                          L-myc pseudogene.";
Genes Dev. 1:1311-1326(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M19720; AAA59879.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07262; CAA30248.1; -. EMBL; X07263; CAA30249.1; -. EMBL; AL033527; CAB75682.1; PIR; A27675; TVHUML.
                                                                          83.7%;
                                                         2438 MW;
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TRANSFAC; T02385; -.
Genew; HGNC:7555; MYCL1.
                                                                   Query Match
Best Local Similarity 71...
5; Conservative
    1
13
14
15
                                                                                                                                                                                                                                      MYCLI OR MYCL OR LMYC.
                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                 CDKDFYR 15
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11
13
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20 AA;
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VARIANT
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SEQUENCE
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VARIANT
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBUNIT: Efficient DNA binding requires dimerization with another bHLH protein. Binds DNA as an heterodimer with MAX.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-! SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legouy E., DePinho R.A., Zimmerman K., Collum R., Yancopoulos G.D., Mitsock L., Kriz R., Alt F.W.; "Structure and expression of the murine L-myc gene."; EMBO J. 6:3359-3366(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 364;
Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                    HELIX-LOOP-HELLY MOTIF.
LEUCINE-ZIPPER (POTENTIAL).
S -> T (IN REF. 3).
58F8A71A1C2ED6D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                       PROSITE; PS50888; HLH; 1.
Nuclear protein; DNA-binding; Proto-oncogene.
DNA BIND 282 294 BASIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=88111523; PubMed=2828024;
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                          40312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-myc proto-oncogene protein.
MYCL1 OR MYCL OR LMYC1.
Pfam, PF00010; HLH; 1.
Pfam; PF01056; Myc N term; 1.
PRINTS; PR00044; LEUZIPPRMYC.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 85.7
nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                      361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CGEDFYR 21
                                                                                                                                                                                                                                                                                                                                                                                                          364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CEEDFYR 7
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                                                                                                                                                                                                                                                   282
295
333
362
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P10166;
                                                                                                                                                                                                                                                                                                                              DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                    DOMAIN
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MEDLINE-21291005; PubMed=11397841;
MEDLINE-21291005; PubMed=11397841;
MEDLINE-21291005; PubMed=11397841;
MEDLINE-21291005; PubMed=11397841;
Medlious M., Merkovitz G.D., McElreavey K.;
"Absence of mutations involving the LiM homeobox domain gene LHX9 in 46, XY gonadal agenesis and dysgenesis.";
J. Clin. Endocrinol. Metab. 86:2465-2469(2001).
--- FUNCTION: Involved in gonadal development (By similarity).
--- SUBCELLULAR LOCATION: Nuclear (Probable).
--- SIMILARITY: Contains 1 homeobox domain.
--- SIMILARITY: Contains 2 LIM zinc-binding domains.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Nuclear protein; DNA-binding; Proto-oncogene.

Nuclear protein; DNA-binding; Proto-oncogene.

DNA BIND 286 298 BASC DOWAIN.

DOWAIN 337 365 LEUCINE-ZIPPER (POTENTIAL).

SRQUENCE 368 AA; 40848 MW; 9174F6FD7C03321E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHX9 HUMAN STANDARD; PRT; 388 AA. Q9NQ65; Q9BYU6; Q9NQ70; 16-OCT-2001 (Rel. 40, Created) 28-FEB-2003 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) LIM/homeobox protein Lhx9.
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EMBL, AJ277916; CAB98128.1; ALT SEQ.
EMBL, AJ277917; CAB98128.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96799; Lmyc1.
InterPro; 1PR001092; HIH basic.
InterPro; 1PR002418; TF_Myc.
Pfam; PP00010; HIH; 1.
Pfam; PR01056; Myc N term; 1.
PRINTS; PR00044; LEUZIPPRNYC.
SMART; SM00353; HIH; 1.
                                                                                                                                                                                                                                          EMBL, X13945; CAA32128.1; -. EMBL, BC053059; AAH53059.1; PIR; S03017; TVMSML. HSSP, P25912; 1HLO. TRANSPAC; T02387; -.
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Best Local Similarity
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   Db
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"Characterization of Lhx9, a novel LIM/homeobox gene expressed by the pioneer neurons in the mouse cerebral cortex."; Mech. Dev. 81:193-198(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Retaux S., Rogard M., Bach I., Failli V., Besson M.J.,
"Lhx9: a novel LIM-homeodomain gene expressed in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=21021315; PubMed=10756098;
Failli V., Rogard M., Mattei M.-G., Vernier P., Retaux S.;
"Lhx9 and Lhx9alpha LIM-homeodomain factors: genomic structure, expression patterns, chromosomal localization, and phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%; Score 36; DB 1; Length 388; 71.4%; Pred. No. 12; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 177 LIM 2.
258 317 HOMEOBOX.
388 AA; 42903 MW; A4DC8B914D7C3B66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHX9 MOUSE STANDARD; PRT; 388 AA. Q9WUH2; Q9QWQ6; Q9QZ00; Q9WU44; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) LIM/homeobox protein Lhx9.
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LIM 2.
HOMEOBOX.
                                           JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00478; LIM DOMAIN 1; 2. PROSITE; PS50027; LIM DOMAIN 2; 2. PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS0071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
InterPro; IPR001701; LIM. homeo.
Pfam; PP00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
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AJ277918; CAB98128.1;
AJ277919; CAB98128.1;
AJ277920; CAB98128.1;
AJ296272; CAC33174.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 11-388 FROM N.A.
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                                                                                                                                                      HSSP, P06601; 1FJL.
Genew, HGNC:14222; LHX9.
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177
317
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111 CKEDYYR 117
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LHX9_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VWFQNARAKFRRNLLRQENGGVDKADGTSLPAPPSADSGAL
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R SMART; SM00132; HOX; 1.
R SMART; SM00132; LIM; 2.
DR PROSITE; PS00071; HOMEOBOX_1; 1.
DR PROSITE; PS00071; HOMEOBOX_2; 1.
DR PROSITE; PS00073; LIM DOMAIN_1; 2.
DR PROSITE; PS00073; LIM DOMAIN_1; 2.
KW HOMEOBOX; DNA-binding; Nuclear protein; Repeat; LIM domain; KW Metal-binding; Zinc; Alternative splicing.

**Alternative splicing.**
**Ind 1.
**Ind 2.**
**Ind 2.**
**Ind 3.**
**Ind
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Pred. No. 12;
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-> F (IN REF. 2).
C2D7326A68D87B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 homeobox domain. SIMILARITY: Contains 2 LIM zinc-binding domains.
analysis.";
Genomics 64:307-317(2000).
-!- FUNCTION: Involved in gonadal development.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP 003111.
                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9WUH2-2; Sequence=VSP 003111;
                                                                                                                                                                                                                                                                                            IsoId=Q9WUH2-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMEL, AF113518, AAD22008.1;
EMEL, AJ243851, CAB59907.1;
EMEL, AJ243852, CAB59907.1;
EMEL, AJ243853, CAB59908.1;
EMEL, AJ243854, CAB59908.1; JOINED.
EMEL, AJ243855, CAB59908.1; JOINED.
EMEL, AJ243855, CAB59908.1; JOINED.
EMEL, AJ243853, CAB59908.1; JOINED.
EMEL, AJ243853, CAB59908.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ243854; CAB59909.1; JOINED.
AJ243855; CAB59909.1; JOINED.
AJ243857; CAB59909.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1316721; Lhx9.
InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LiM.
InterPro; IPR07107; LiM.homeo.
Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF134761; AAD30110.1; -.
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388 AA; 42986 MW;
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71.4%;
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TRANSFAC; T04192; -.
TRANSFAC; T04195; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
153
                                                                                                                                                                                                                                                          Name=Beta;
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CONFLICT
SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain cortex;

Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Kawakami B., Sugiyama A., Takemoto M., Ishii S., Yamamoto J., Isono Y.,

Kawai-Hio Y., Saito K., Niahikawa T., Kimura K., Yamashita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,

Murakawa K., Kanehori K., Takahashi-Pulii A., Oshima A., Suzuki Y.,

Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

"NEDO human cDNA sequencing project.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 18-406 FROM N.A.
MEDIANE=99162575; PubMed=10051612;
Rincon-Limas D.E., Lu C.-H., Canal I., Calleja M.,
Rodriguez-Esteban C., Izpisua-Belmonte J.-C., Botas J.;
"Conservation of the expression and function of apterous orthologs in
                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=9625351; PubMed=6649822;
MEDLINE=9625351; PubMed=6649822;
Wu H.-K., Heng H.H.Q., Siderovski D.P., Dong W.-F., Okuno Y.,
Shi X.-M., Tsui L.-C., Minden M.D.;
Shi X.-M., Tsui L.-C., Minden M.D.;
"Identification of a human LIM-Hox gene, hIH-2, aberrantly expressed
"Identification of a human LIM-Hox gene, hIH-2, aberrantly expressed
in chronic myelogenous leukaemia and located on 9433-34.1.";
                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila and mammals.",

Proc. Natl. Acad. Sci. U.S.A. 96:2165-2170 (1999).

-!- FUNCTION: Transcriptional regulatory protein involved in the control of cell differentiation in developing lymphoid and neural cell types (By similarity).

-!- SUBCELDIULAR LOCATION: Nuclear (Probable).

-!- SIMILARITY: Contains 1 homeobox domain.

-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
LHX2 HUMAN

ID _ LHX2 HUMAN

TO _ LOG458; O95860; Q8N1Z3;

DT _ 10-OCT-1996 (Rel. 34, Created)

DT _ 30-MAY-2000 (Rel. 39, Last sequence update)

DT _ 10-OCT-2003 (Rel. 42, Last annotation update)

DT _ 10-OCT-2003 (Rel. 42, Last annotation update)

DE _ LIM/homeobox protein Lhx2 (Homeobox protein LH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U11701; AAB08752.1; -.
EMBL; AK094511; BAC04371.1; ALT_INIT.
EMBL; AF124735; AAD20013.1; -.
HSSP; P06601; IFJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; 1. Pfam; PF00412; LIM; 2. ProDom; PD000010; Homeobox; 1. ProDom; PD000094; LIM; 2. SMART; SM00389; HOX; 1. SMART; SM0132; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
InterPro; IPR007107; LIM_homeo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 4-406 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T01967; -. Genew; HGNC:6594; LHX2.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 603759;
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.. 0

Gaps

.. 0

Indels

Mismatches

5:

Conservative

Local Similarity

Matches

|:||:|| 111 CKEDYYR 117

CEEDFYR 7

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InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                   168
196
325
323
                                                                                                                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                          Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 CKEDYYR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CEEDFYR
                                                                                                                                                                                                                                                                                                                                            53
115
187
266
307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHX2 OR LH2.
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DOMĀIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                            A -> Q (IN REF. 1).

AAA -> RAR (IN REF. 1).

BASING (IN REF. 1).

NA -> TR (IN REF. 1).

GHEPHSPSQTTLINLE -> AMSLTAPHKRLLPTFSNDSQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE 99162575; PubMed=10051612; Rincon-Limas D.E., Lu C.-H., Canal I., Calleja M., Rincon-Limas D.E., Lu C.-H., Canal I., Calleja M., Rodriguez-Esteban C., Izpisua-Belmonte J.-C., Botas J.; "Conservation of the expression and function of apterous orthologs in Drosophila and mammals."; Proc. Natl. Acad. Sci. U.S.A. 96:2165-2170(1999).

-!-FUNCTION: Transcriptional regulatory protein involved in the control of call differentiation in developing lymphoid and neural
                                                                                                                                                                                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

A -> GENGRER (IN REF. 1).

A -> G (IN REF. 1).

Y -> YSPSIHGPY (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o
O
; PS00478; LIM DOMAIN 1; 2.
; PS50023; LIM DOMAIN 2; 2.
; PS00027; HOMBOBOX 1; 1.
; PS50071; HOMBOBOX 2; 1.
x; DNA-binding; Nuclear protein; Repeat; LIM domain; inding; Zinc; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%; Score 36; DB 1; Length 406; 71.4%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            PHPTISLKKKLSLV (IN REF. 1)
DF73AAC81867D30D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell types (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Probable)
-!- SIMILARITY: Contains 1 homeobox domain.
-!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
36-FEB-2003 (Rel. 41, Last annotation update)
LIM/homeobox protein Lhx2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC, T01969; -. MGD; MGI:96785; Lhx2. GO; GO:0007498; P:mesoderm development; IMP. GO; GO:0007399; P:neurogenesis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                 POLY-ALA. HOMEOBOX.
                                                                                                                                    LIM 1.
LIM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                44373 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF124734; AAD20012.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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196
325
323
323
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107
1187
1196
242
406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                 Metal-binding;
DOMAIN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHX2 MOUSE
Q9Z0S2;
                                                                                             Homeobox;
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DNA BIND
DOMAIN
                           PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: Found in discrete regions of the developing CNS, primarily in diencephalic and telencephalic structures and a subset of lymphoid tissues. Also found in embryonic spinal chord and fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=93126348; PubMed=7678338;
Xu Y., Baldassare M., Fisher P., Rathbun G., Oltz E.M.,
Yancopoulos G.D., Jessell T.M., Alt F.W.;
"LH-2: a LiM/homeodomain gene expressed in developing lymphocytes and neural cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 90:227-231(1993).
-!- FUNCTION: Transcriptional regulatory protein involved in the control of cell differentiation in developing lymphoid and neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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R InterPro; IPR001781, LIM.

R InterPro; IPR001707; LIM homeo.

R Pfam; PF0004612; LIM; 2.

R ProDom; PD00001094; LIM; 2.

R ProDom; PD000094; LIM; 2.

R SMART; SM00139; HOX; 1.

R SMART; SM00132; LIM; 2.

R PROSITE; PS00013; LIM DOMAIN 1; 2.

R PROSITE; PS00012; LIM DOMAIN 2; 2.

R PROSITE; PS00012; HOMEOBOX 2; 1.

R PROSITE; PS00012; HOMEOBOX 2; 1.

R PROSITE; PS00012; HOMEOBOX 2; 1.

R HOMEOBOX 2; Nuclear protein; Repeat; LIM domain; Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 406;
Pred. No. 12;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FE7B4E76454D6A90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
LIM/homeobox protein Lhx2 (Homeobox protein LH-2)
                                                                                                                                                                                                                                                                                                                Transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 AA.
                                                                                                                                                                                                                                                                                                                                                                                 POLY-ALA. HOMEOBOX.
                                                                                                                                                                                                                                                                                                                         LIM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    44419 MW;
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71.48;
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Kaneko T., Nakamura Y., Sato S.,
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Best Local Similarity 83...
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CEDDFY 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CEEDFY 6
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48
77
84
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                                                                                                      thaliana.";
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ZN FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
DC8FA3DB4572BB40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·;
                                                                                                                                                                                                                         PROSITE: PS00027; HOMBOBOX 1; 1.
PROSITE; PS000478; LIM DOMAIN 1; 2.
PROSITE; PS50023; LIM DOMAIN 2; 2.
PROSITE; PS5001; HOMEDBOX 2; 1.
HOMBOBOX; DMA-binding; Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Transcription regulation.
52 104 LIM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         83.7%; Score 36; DB 1; Length 426; 71.4%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                        LIM 2.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc finger protein constans-like 11.
AT3G07650 OR MLP3.10.
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MEDLINE=21016720; PubMed=11130713;
                    EMBL; L06804; -; NOT_ANNOTATED_CDS
HSSP; P06601; 1FJL.
                                                                                                                      Pfam; PF00046; homeobox; 1.
Pfam; PF00412; LIM; 2.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000094; LIM; 2.
SWART; SM00389; HOX; 1.
SWART; SM00132; LIM; 2.
                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
InterPro; IPR007107; LIM.homeo.
                                                                                                                                                                                                                                                                                                                                                                                                        47418 MW;
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101 CKEDYYR 107
                                                                                                                                                                                                                                                                                                                                                                                       305 3
426 AA;
                                                    TRANSFAC; T01966; -
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CEEDFYR 7
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (BAL (Bile-salt-stimulated lipase) (ResL) (Carboxyl ester lipase) (Sterol esterase) (Cholesterol esterase) (Pancreatic lysophospholipase).
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MEDLINE=96679098; PubMed=8530060;
Lidmer A.S., Kannius M., Lundberg L., Bjursell G., Nilsson J.;
imolecular cloning and characterization of the mouse carboxyl ester lipase gene and evidence for expression in the lactating mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUB-Mammary gland;
MEDLINE=96096531; PubMed=8522186;
Mackay K., Lawn R.M.;
"Characterization of the mouse pancreatic/mammary gland cholesterol esterase-encoding onNa and gene.";
Gene 165:255-259(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                              Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence and analysis of chromosome 3 of the plant Arabidopsis
Kato T., Asamizu
K., Kishida Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1; Length 372; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50119; ZF BBOX; 2.
Zinc-finger; Nuclear protein; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188F18EB283D7479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B BÖX-TYPE 1.
B BOX-TYPE 2 (ATYPICAL).
POLY-ASN.
                                                                                                                                                                                                                                                         Nature 408:820-822(2000).

-:- SUBCELLULAR LOCATION: Nuclear (Potential).

-:- SIMILARITY: Belongs to the CONSTANS family.

-:- SIMILARITY: Contains 2 B box-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC009176; AAF13083.1; -.
InterPro; IPR000315; Znf_Bbox.
InterPro; IPR002926; Znf_constans.
Pfam, PF00643; Zf-B_box; 2.
ProDom; PD007661; Znf_constans; 1.
SMART; SM00336; BBOX; 2.
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Repeat; Signal
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                            4 X 11 AA TANDEM REPEATS, O-GLYCOSYLATED REGION.
                                                                                                SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEL_RAT STANDARD; PRT; 612 AA.
P07882; P14722;
01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bile-salt-activated lipase precursor (EC 3.1.1.3) (EC 3.1.1.13) (BAL)
(Bile-salt-stimulated lipase) (BSL) (Carboxyl ester lipase) (Sterolesterase) (Cholesterolesterase) (Pancreatic lysophospholipase).
         JUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT WITH PANCREATIC LIPASE AND COLIFASE FOR THE COMPLETE DIGESTION OF DIETARY TRIGLYCERIDES (BY SIMILARITY).

CATALYTIC ACTIVITY: Triacy1glycerol + H(2)O = diacy1glycerol + i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                fatty acid anion.
CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
9E4428FDFCA8602E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                         Pfam; PF00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; Length 599;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BILB-SALT-ACTIVATED LIPASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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EMBL, U37386; AAC52279.1; --
PIS; P57701; AA57701.
HSSP, P30122; 2BCE.
SWISS-2DPAGE; Q64285; MOUSE.
MGD; MG1:88374; Cel.
GO; GO:0046514; P:ceramide catabolism; IMP.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR003779; Ser_estrs.
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581
207
325
599 AA;
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AA POINT
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DT 011-1
DT 011-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group.
-!- TISSUB SPECIFICITY: SYNTHESIZED PRIMARILY IN THE PANCREAS AND THEN TRANSPORTED TO THE INTESTINE.
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ENZYME REGULATION: Activated by bile salts containing a 7-hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVE SITE HIS-455.

MEDLINE=91154187; PubMed=1999399;

MEDLINE=91154187; PubMed=1999399;

Dispersio L.P., Fontaine R.N., Hui D.Y.;

"Site-specific mutagenesis of an essential histidine residue in pancreatic cholesterol esterase.";

J. Biol. Chem. 266.4033-4036(1991).

-!- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION OF DIETARY TRIGLYCERIDES.

-!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
                                                                                                                                                                                                                                                                                                                                                                        Han J.H., Stratowa C., Rutter W.J.;
"Isolation of full-length putative rat lysophospholipase cDNA using improved methods for mRNA isolation and cDNA cloning.";
Biochemistry 26:1617-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVE SITE SER-214.
MEDLINE=91009095; PubMed=2211595;
Dipersio L.P., Fontaine R.N., Hui D.Y.;
"Identification of the active site serine in pancreatic cholesterol esterase by chemical modification and site-specific mutagenesis.";
". Biol. Chem. 265:16801-16806(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: A steryl ester + H(2)0 = a sterol + a fatty
                                                                                                                    Kissel J.A., Fontaine R.N., Turck C.W., Brockman H.L., Hui D.Y., "Molecular cloning and expression of cDNA for rat pancreatic cholesterol esterase." Biochim. Biophys. Acta 1006:227-237(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=91299758; PubMed=2069957;
Fontaine R.N., Carter C.P., Hui D.Y.;
"Structure of the rat pancreatic cholesterol esterase gene.";
Biochemistry 30:7008-7014(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BILE-SALT-ACTIVATED LIPASE
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SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Pancreas;
MEDLINE-90089378; PubMed-2688744;
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EMBL; M49157; AAB461376.1; --
PINE, A34967; A34967.
HSSP; P30122; 2BCE.
InterPro; IRR002018; CarbesteraseB.
InterPro; IRR003019; Ser_estrs.
Pfam; PP00135; COesterase; 1.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=87242339; PubMed=3593682;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrence 269:496-512(L995).
-!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside triphosphate + oxidized
thioredoxin + H(2)0 = ribonucleoside triphosphate + reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
    BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

4 X 11 AA TANDEM REPEATS, O-GLYCOSYLATED

REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Ngryen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Tetramer consisting of 2 alpha (NrdD) and 2 beta (NrdG) subunits (By similarity).
-!- SIMILARITY: STRONG, TO E.COLI AND T4 NRDD.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                      H-SQ, R, A, S, D: ABOLISHES ACTIVITY.
V -> L (IN REF. 2).
G -> A (IN REF. 2).
S -> I (IN REF. 2).
S -> I (IN REF. 2).
T -> M (IN REF. 2).
T -> M (IN REF. 3).
GG -> VV (IN REF. 3).
GG -> VA (IN REF. 3).
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0
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2).
NRDD OR HI0075.
                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 612;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                     0; · Indels
                                                                                                                          H->Q: NO EFFECT ON ACTIVITY
                                                                                                                                                                                                                                                                                1569CE4EA71ED02A CRC64;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                 67040 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                           Query Match 79.1
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
                                                                                                                                          455
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608
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612 AA;
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SEQUENCE
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           Length 707;
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53;
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                                                                                                                      Score 34;
Pred. No.
or send an email to license@isb-sib.ch)
                                                                                                                                                                                            completed: June 9, 2004, 15:49:06
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                                                                                                                                                                                                     : 6.10811 secs
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                                                                                                                        Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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9, 2004, 15:43:00 ; Search time 23.4595 Seconds - protein search, using sw model June OM protein Run on:

(without alignments) 94.147 Million cell updates/sec US-09-660-302D-7

1 CEEDFYR 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 segs, 315518202 residues

1017041 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_25:* Database

sp archea:*
sp bacteria:*
sp bunga:*
sp funga:*
sp human:*
sp mammal:*
sp mycrebrate:*
sp organelle:* unclassified: * sp_vertebrate:* sp_bacteriap:* sp plant:*
sp_rodent:*
sp_virus:* rvirus: 10: 112: 123: 14: 15: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΠD	OBRAGE	D95ML5	1ZSX6C	08VC07	08C356	29U9B1	016938	O98SF6	014897	098SE7	081124	0865X9	090881	OBOMBO	SETH2	042108
	DB	16	9	9	11	H	'n	'n	13	4		11	9	13	1	4	13
	Query Match Length DB	153	632	638	399	399	76	91	125	206	217	325	369	378	388	397	400
de	Query Match	88.4	88.4	88.4	86.0	86.0	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7
	Score	38	38	38	37	37	36	36	36	36	36	36	36	36	36	36	36
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632 AA.

PRT;

PRELIMINARY;

RESULT 2 Q95ML5 ID Q95ML5 AC Q95ML5;

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CEEDFY 21

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	Q8idq5 plasmodium Q8ivq6 homo sapien Q16939 ancylostoma Q8df30 vibrio vuln Q9w4q9 drosophila
Q9M9Y2 Q9PNX2 Q8S056 Q8S056 Q8S227 Q26638 Q26638 Q8DZ48 Q8UXV2 Q8UXV2 Q8ISX6 Q8SUG6 Q9XIII Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III Q97III	Q8IDQ5 Q8IVG6 Q16939 Q8DF30 Q9W4Q9
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88.4%; Score 38; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                         Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 153 AA; 18428 MW; 3B0F4ED430B1A0FA CRC64;
                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein TTE2033.
                        153 AA
                       PRT;
                      PRELIMINARY;
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STRAIN=C57BL/6J; TISSUB=Lung;
STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINET=22354683; PubMed=12466851;
The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK086863; BAC39755.1; -.
EMBL; AK086883; BAC39755.1; -.
EMBL; AK086883; BAC39755.1; -.
EMBL; PRO07529; Znf_HIT.
Fram; PPO4488; zf_HIT; 1.
Fram; PPO4488; zf_HIT; 1.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 32;
0; Mismatches 1; Indels
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InterPro; IPR007529; Znf_HIT.
Pfam; PF04438; Zf-HIT; 1.
SEQUENCE 399 AA; 42995 MW; B5CA88342B56932B CRC64;
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01-MAR-2002 (TYEMBLrel. 2:
01-MAR-2002 (TYEMBLrel. 2:
01-JUN-2003 (TYEMBLrel. 2:
Open reading frame 6:
ORP6.
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002966; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
FINTERPO; IPR0039528; Hemtopoptn_L_FI.
                                                                                                                                                                                                                                                                                                                                               .; IEA
                                                                                                                                                                                      X MEDLINE-21265430; PubMed=11371582;
X MEDLINE-21265430; PubMed=11371582;
X ALIU J.C., Makvak R.D., Adkins R.M., Gibson S., Li W.H.;
This social Evolution of Growth Hormone in Primates and Emergence of the Species Specificity of Human Growth Hormone Receptor.";
Mol. Biol. Evol. 18:945-953(2001).
II Mol. Biol. Evol. 18:945-953(2001).
R GO, GO:00166020; Camembrane; IEA.
R GO; GO:00166020; Camembrane; IEA.
R GO; GO:00166020; Camembrane; IEA.
R GO; GO:00166020; F:hematopoietin/interferon-class (D200-domain. . .; IEZ)
R GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEZ)
R InterPro; IPR003961; FN_III.
R InterPro; IPR003589; Hemtopoptn_L.F1.
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MEDLINE=99367319; PubMed=10425448;
MEDLINE=99367319; PubMed=10425448;
Zogopoulos G., Nathaniels P., Hendy G.N., Goodyer C.G.;
The baboon: a model for the study of primate growth hormone receptor gene expression during development.";
J. Mol. Endocrinol. 23:67-75(1999)."
EMBL; AF150751; AAD39536.1;
HSSP; P10912; 1AXI.
                                                                                     Saimiri boliviensis (Bolivian squirrel monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Platyrrhini; Cebidae, Cebinae, Saimiri.
NCBI_TaxID=27679;
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Growth hormone receptor.
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100.0%; Pred. No. 32;
iive 0; Mismatches
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PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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Papio anubis (Olive baboon)
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Pfam; PF00041; fn3;
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125 AA;
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CKEDYYR 34
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"Anticoagulant repertoire of the hookworm Ancylostoma caninum.";
Proc. Natl. Acad. Sci. U.S.A. 93:2149-2154(1996).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Ascaris type serine procease inhibitor (Fragment).
Ancylostoma ceylanicum.
Eukaryota; Metazoa: Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostoma.
NCBI_TAXID=53326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harrison L.M., Cappello M.;
"The molecular cloning of an ascaris type serine protease inhibitor from adult Ancyloseroma ceylanicum hookworms.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
BMBL; AR172653; AAD51346.1; -.
HSSP; P56682; ICCV.
GO; GO:000823; F:peptidase activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR0052099; TIL_Cysrich.
Pfam; PF01826; IIL; 1.
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01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Anti-coaqulant protein C2 precursor (Fragment).
Ancylostoma caninum (Dog hookworm).
Bukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatcidaa; Ancylostomatidae; Ancylostoma.
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Pred. No. 9.6;
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                                                                                                                                                                                                             76 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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SEQUENCE FROM N.A.
MEDLINE=96312555; PubMed=8700900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
76 AA; 8385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 85.7
les 6; Conservative
                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                 | ||||||
CAEDFYR 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 CEEGFYR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CEEDFYR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
   CEEDFYR
                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q16938
Q16938;
                                                                                                                                     RESULT 6
099991
1D 091991
AC 09999
DT 01-M
DT 
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216938
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"The LIM-homeodomain family in the developing xenopus brain:
conservation and divergences with the mouse related to the evolution
of the forebrain.",
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Pred. No. 16;
2; Mismatches 0; Indels
                                                                                                                                                                                                                               Length 91;
                                                                                                                                                               ANTI-COAGULANT PROTEIN C2.
ECB11CB4597C24DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14283 MW; 375E42A29104D364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Lhx2 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                       83.7%; Score 36; DB 5;
85.7%; Pred. No. 12;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA.
                                                                                                                                            POTENTIAL.
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PROSITE; PS00478; LIM DOMAIN 1; 1.
PROSITE; PS50023; LIM DOMAIN 2; 2.
LIM domain; Metal-binding; Zinc.
NON TER 125 125
SRQUENCE 125 AA; 14283 WW; 37584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
PDB; 1COU; 13-OCT-99.
InterPro; IPR006209; EGF like.
InterPro; IPR002919; TIL_Cysrich.
Pfam; PP01826; TIL; 1.
PROSITE; PS01186; EGF_2; 1.
                                                                                                                   1 7 8 91 AA; 10358 MW; F 83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.78;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ311712; CAC35215.1;
HSSP; P32965; 1CTL.
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001781; LIM.
Pfam; PF00412; LIM; 2.
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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01-NOV-1996 (
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Query Match 83.7
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                Query Match
Best Local Similarity 71.4
Matches 5; Conservative
  ProDom; PD000094; LIM; 2.
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                                                                                                                                                                                                                           27 CKEDYYR 33
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                                                                                                                                                                                                  1 CEEDFYR 7
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SEQUENCE
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Q811Z4
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the forebrain.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY; CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ311711; CAC35214.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006375; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001356; Homeobox.

InterPro; IPR001781; LIM.

Pfam; PF004045; homeobox; 1.

ProDom; PD000010; Homeobox; 1.
                                                                                                                                   Kaye F., Battey J., Nau M., Brook B., Seifter E., De Greve J., Birrer M., Sausville E., Minna J.;
"Structure and expression of the human L-myc gene reveal a complex pattern of alternative mRNA processing.";
Mol. Cell. Biol. 8:186-195(1988).
                                                                                                                                                                                                                                                                                    EMBL; BCUllows, ...
TRANSFAC; T02386; -.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003700; F:transcription factor activity; NAS.
GO; GO:000355; P:regulation of transcription, DNA-dependent; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
EARLY FPO1056; Myc N term; 1.
PRINTS; PR00044; LEUZIPPRMYC.
FEAN; PR01056; Myc N term; 1.
FRINTS; PR00044; LEUZIPPRMYC.
-- '. I.enqth 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
L-myc protein (Similar to lung carcinoma myc related oncogene 1) L-MYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

83.7%; Score 36; DB 4; Length 206;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL-2001) to the BMBL/GenBank/DDBJ databases.
EMBL; M19720; AAA59878.1; -.
EMBL; BC011864; AAH11864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 AA.
                                                                                                                            MEDLINE=88094386; PubMed=2827002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lhx9 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 CGEDFYR 21
                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CEEDFYR 7
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    TISSUE=Placenta;
                                                                                                                   TISSUE=Placenta;
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Mazaud S., Oracal B., Guigon C.J., Carre-Eusebe D., Magre S.;
Mazaud S., Oracal B., Guigon C.J., Carre-Eusebe D., Magre S.;
LIAS expression during gonadal morphogenesis as related to the state of cell differentiation.",
Gene Expr. Patterns 2:373-377 (2002).
Gene Expr. Patterns 2:373-377 (2002).
Gene Expr. Patterns 2:373-377 (2002).
GO; GO:0005544; Crucleus; IEA.
GO; GO:00055644; Crucleus; IEA.
GO; GO:0005555; P:requilation of transcription, DNA-dependent; IEA.
GO; GO:0005555; P:requilation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                              83.7%; Score 36; DB 13; Length 217; 71.4%; Pred. No. 27; cive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LIM-homeodomain type transcription factor Lhx9 (Fragment).
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                   217 217 217 24716 MW; 6CBE88B595ECB851 CRC64;
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2; Mismatches
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InterPro; IPR001356; Homeobox.
InterPro; IPR001781; LIM.
InterPro; IPR001781; LIM.
InterPro; IPR001701; LIM homeo.
Pfam; PP000046; homeobox; 1.
ProDom; PD000094; LIM; 2.
ProDom; PD000094; LIM; 2.
ProDom; PD000094; LIM; 2.
PRODOM; PR000139; LIM; 2.
PROSITE; PS00027; HOWEOBOX 1; 1.
PROSITE; PS00027; HOWEOBOX 2; 1.
PROSITE; PS00021; HOWEOBOX 2; 1.
PROSITE; PS00021; LIM DOMAIN 1; 2.
PROSITE; PS00021; LIM DOMAIN 1; 2.
PROSITE; PS00021; LIM DOMAIN 2; 2.
PROSITE; PS00021; LIM DOMAIN 2; 2.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q811Z4;
01-JUN-2003 (TrEMBLrel. 24, Created)
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SMART; SM0389; HOX; 1.
SMART; SM00132; LIM; 1.
SMOSITE; PSS0071; HOMEDOX 2; 1.
PROSITE; PS00478; LIM DOWAIN 1; 1.
PROSITE; PS50023; LIM DOMAIN 2; 1.
LIM domain; Metal-binding; Zinc.
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71.48;
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83.7%;
71.4%;
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Best Local Similarity 71.4%,
'-hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.*
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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101 CKEDYYR 107
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                                                                                                                                                                                                 Paradis V.R., Forget C.L., Silversides D.W.;

Bas scrofa Linx9 mRNA.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

R BMBL; AX240553, AA085392.1;

R GO; 60010056534; C:nucleus; IEA.

R GO; GO:0006355; P:regulation factor activity; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001356; Homeobox.

R InterPro; IPR001107; LIM.

R Pfam; PF00042; LIM.

R Pfam; PF000412; LIM.

R ProDom; PD0000101; Homeobox; 1.

R ProDom; PD000094; LIM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.7%; Score 36; DB 6; Length 369; 71.4%; Pred. No. 47; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41025 MW; 9C8FA3ADF572F9AE CRC64;
               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
LIM-homeobox protein 9 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM0389; HOX; 1.
SMART; SM00139; LIM; 2.
PROSITE; PS00027; HOMEDBOX 1; 1.
PROSITE; PS50071; HOMEDBOX 2; 1.
PROSITE; PS50073; LIM DOWAIN 1; 2.
PROSITE; PS50073; LIM DOWAIN 2; 2.
DNA-binding; HOM DOWAIN 2; 2.
NON_TER 369 369 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L35566; AAA50258.1; -.
PIR; JC5658; JC5658.
HSSP; P32965; 1CTL.
GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LH-2.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||:||
120 CKEDYYR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 AA;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CEEDFYR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homeobox protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090881
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Matches
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Et anscription factor Libro...

Example: Av273890; AAP32472.1; -..

EMBL; Av273890; AAP32472.1; -..

CO; GO:00053700; Fitranscription factor activity; IEA.

Example: Example
R GO; GO:0003700; F:transcription factor activity; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001356; Homeobox.

R InterPro; IPR001707; LIM_homeo.

R Pfam; PF00046; homeobox; 1.

R Pfam; PF00046; homeobox; 1.

R Probom; PD000010; Homeobox; 1.

R Probom; PD000010; Homeobox; 1.

R Probom; PD000010; Homeobox; 1.

R PROSTIF; SM00132; LIM; 2.

R PROSTIF; PS00027; HOMEOBOX 1; 1.

R PROSTIF; PS00027; HOMEOBOX 1; 1.

R PROSTIF; PS00011; HOMEOBOX 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00478; LIM DOWAIN 1; 2.
PROSITE; PS50023; LIM DOWAIN 2; 2.
DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.7%; Score 36; DB 13; Length 378; 71.4%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shan Y.X., Pan J., Geng D.C., Gu M.Y., Yu L., "Cloning and characterization of Rat LIM-homeodomain type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 378 AA; 42007 MW; 34220850FCE82FFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-07T-2003 (TrEMBLrel. 25, Last annotation update)
LIM-homeodomain type transcription factor Lhx9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 49;
2; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 CKEDYYR 117
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RESULT 15

Q86UH2

DC 086UH2;

C 086UH2;

DC 01-0CT-2003 (TrEMBLrel. 24, Created)

DT 01-0CT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-0CT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)

DE LIM-homeobox 9 protein.

S Homo sapiens (Human).

C EUKARYOCTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

C Mammalia; Eutheria; Primata; Craniata; Vertebrata; Homo.

OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=9606;

RN [1]

RP SQUENCE FROM N.A.

RA Shan V.X., Pan J. Guo Z.K., Geng D.C., Huang C.O., Yu L.;

RA Shan V.X., Pan J. Guo Z.K., Geng D.C., Huang C.O., Yu L.;

RY "Cloning and characterization of human novel LIM-homeobox 9 gene.";

RY "Cloning and characterization of human novel LIM-homeobox 9 gene.";

RY "Cloning and characterization of human novel LIM-homeobox 9 gene.";

RY "Cloning and AP32471.2;

CLONA, DNA-binding; Homeobox; Nuclear protein.

SQ SEQUENCE 397 AA; 43976 MW; FA8BBBSSOASFCE03 CRC64;

AURA-binding; Homeobox; Nuclear protein.

SQ SEQUENCE 397 AA; 43976 MW; RABBBSSOASFCE03 CRC64;

Autches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

ALCEDPEYR 7

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DD 120 CKEDPYR 126
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Search completed: June 9, 2004, 15:51:24 Job time: 25.4595 secs